us-10-623-189-1.rag

Tue May

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GenCore version 5.1.7
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- protein search, using sw model OM protein May 4, 2006, 21:46:23 ; Search time 138.474 Seconds Run on:

(without alignments)
463.258 Million cell updates/sec

US-10-623-189-1 Perfect score: Title:

736 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 146 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 seqs, 439378781 residues Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneeqp1980s:* geneeqp1990s:* geneeqp2000s:* geneeqp2001s:* geneeqp2001as:* geneeqp2003as:* geneseqp2004s:* geneseqp2005s:* A_Geneseq_21:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result	ק ק	Query	* Query Match Length DB	EC BC	10	Description
	3005	110001	The state of	3		
-	736	100.0	146	8	AAW00013	Aaw00013 Acid stab
7	736	100.0	146	~	AAR99490	Aar99490 Chimeric
m	736	100.0	146	N	AAW00539	Aaw00539 Human ma
4	736	100.0	146	~	AAW30892	Aaw30892 Synthetic
S	736	100.0	146	N	AAW34482	Aaw34482 Human obe
9	736	100.0	146	~	AAW10151	Aaw10151 Properly
7	736	100.0	146	7	AAW22901	
80	736	100.0	146	7	AAW30791	Aaw30791 Obesity
σ	736	100.0	146	7	AAW26194	Aaw26194 Obesity p
10	736	100.0	146	~	AAW34483	
11	736	100.0	146	7	AAW32575	Aaw32575 Anti obes
12	736	100.0	146	7	AAW34489	Aaw34489 Obesity E
13	736	100.0	146	~	AAW69682	Aaw69682 Human obe
14	736	100.0	146	~	AAW53342	Aaw53342 Obesity p
15	736	100.0	146	~	AAY43311	Aay43311 Human leg
16	736	100.0	146	7	AAY06102	Aay06102 Human obe
17	736	100.0	146	m	AAY92712	Aay92712 Mature
18	736	100.0	146	ო	AAY82111	Aay82111 Mature
19	736	100.0	146	ო	AAY80260	Aay80260 Human mat
20	736	100.0	146	٣	AAY83768	Aay83768 Human OB
21	736	100.0	146	٣	AAY97871	Aay97871 Mature
22	736	100.0	146	m	AAY95786	Aay95786 Mature
23	736	100.0	146	٣	AAY95531	Aay95531 Human mat
24	736	100.0	146	m	AAB14265	Aab14265 Mature hu

Aab70130 Mature hu Aae23614 Human lep Abg32264 Recombina Abp63579 Human obe	Adg65529 Human lep Abr57162 Recombina Adc06694 Leptin ta Add26675 Human adi	~	Adv90297 Protease- Adw96956 Human wil Agw34394 Human Met	Human Human Human Mature	Aaw07192 Human ant Aaw28801 Human mas Aaw71849 Obesity p
AAB70130 AAE23614 ABG32264 ABP63579	ADG65529 ABR57162 ADC06694	ADD71107 AD180474 ADL88877	ADV90297 ADW96956 AAW34394	AAW53328 AAY43314 AAY92261	AAW07192 AAW28801 AAW71849
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ALIGNMENTS

ob protein; adiposity regulating hormone; mouse; acid stability; adsorption characteristic; obesity; type II diabetes; cardiovascular disease; cancer. BE; Schoner Acid stable modified ob protein (Asp22Asn). Heath WF, Location/Qualifiers AAW00013 standard; protein; 146 AA /label= Asp22Asn 95US-00381048. 95US-00383638. 96EP-00300612. Dimarchi RD, (first entry) (ELIL) LILLY & CO BLI. Key Misc-difference Disulfide-bond 29-JAN-1996; 31-JAN-1995; 06-FEB-1995; Basinsky MB, EP725078-A1. 30-SEP-1996 07-AUG-1996. Synthetic RESULT 1 AAW00013

Mammalian derived anti-obesity proteins which regulate fat tissue - used for treating obesity and to reduce risk for type II diabetes, cardiovascular disease and cancer. WPI; 1996-356062/36.

Example 4; Page 19; 42pp; English.

This sequence represents a modified ob proteins. ob proteins are thought to be adiposity regulating hormones. This sequence is based on the mouse ob protein sequence. Proteins such as this have improved stability, egg. acid stability, and improved adsorption characteristics compared to the wild type protein disclosed in Yiying Zhang et al, Nature 372: 425-32

요 ð 셤 ð 셤

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The sequences given in AAB99490-96 represent modified ob proteins which are based on the human ob protein sequence. These protein sequences are covered by the generic sequence given in AAB99489. In these proteins, specific amino acids are substituted for the residues found in the corresponding positions in murine ob protein. These proteins are biologically active for the treatment of obesity, and are more stable than either the murine or human proteins. Individuals treated with these proteins have a reduced risk for type II diabetes, cardiovascular disease and cancer. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
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                   replaced with Lys or
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100.0%; Pred. No. 9e-73;
iive 0; Mismatches 0;
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                                                                                                                                                  note= "Opt. Leu"
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                                                                                                                                                                                                                                                                                                                                        95US-00381048.
95US-00383638.
95US-0000450P.
95US-0002161P.
                   note= "Opt.
                                                                                  'note= "Opt.
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   Misc-difference 106
                                                                                                  Misc-difference 111
                                                                                                                                      Misc-difference 118
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                                   Misc-difference 107
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                                                                    Misc-difference
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06-FEB-1995;
22-JUN-1995;
11-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basinski MB,
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                                                                                                                                                                                                          VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
(December 194). These proteins correspond to the generic formulae given in ARR9947-98). They are biologically active for the treatment of obesity. Individuals treated with these proteins have a reduced risk for type II diabetes, cardiovascular disease and cancer.
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or Val"
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                                                                                                                      DB 2; Length 146;
                                                                                                                  100.0%; Score 736; DB 2; Length 1 ilarity 100.0%; Pred. No. 9e-73; Conservative 0; Mismatches 0; Indels
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Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
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96. .146
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Best Local Similarity
Matches 146; Conserv
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Chimeric.
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AAW30892 standard; protein; 146 AA.
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Matches 146;
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RESULT 4
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                                                                                         Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 736; DB 2; Length 14
100.0%; Pred. No. 9e-73;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halaas JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proenca R, Maffei M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEVVALSRLOGSLODMLWQLDLSPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page ?; 304pp; English.
                                                                                                                                                                                                                                                                                                                   94US-00292345.
94US-00347563.
95US-00438431.
                                                          Human mature obesity protein.
                                                                                                                                                                                                                                                                                  95GB-00016947
                                                                                                                                                                                                                                                                                                                                                                            95US-00483211
                     13-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-099009/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedman JM,
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                  17-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                          10-MAY-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                     17-AUG-1994;
30-NOV-1994;
                                                                                                                                                                                                        GB2292382-A.
                                                                                                                                                                                                                                             21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burley SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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A novel pharmaceutical composition comprises an obesity protein, e.g. the present sequence, together with sucrose and/or trachalose. The composition can be used to treat obesity and associated disorders, e.g. diabetes, cardiovascular disease and cancer. The composition is stable and easy to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDPIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compositions comprising obesity protein - and sucrose
                                                                          sucrose; trehalose; treatment; obesity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obesity protein; therapy; obesity associated disorder; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 736; DB 2;
100.0%; Pred. No. 9e-73;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                               Pikal MJ, Rinella JV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEVVALSRLOGSLODMLWOLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW34482 standard; protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 44; 48pp; English.
                                                                                                  cardiovascular disease; cancer.
                                                                                                                                                                                                                                                                  97EP-00301995
                                                                                                                                                                                                                                                                                                          96US-0014177P.
                                                                                                                                                                                                                                                                                                                              96US-0014951P
(first entry)
                                        Synthetic obesity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Edwards MJ,
                                                                                                                                                                                                                                                                                                                                                                      & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human obesity protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-472913/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or trehalose.
                                                                                 Obesity protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                        (ELIL ) LILLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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AAW10151 is a properly folded intermediate for the production of the biologically active obesity protein AAW22901, which has a similar structure but comprises a disulphide bridge between CY996 and CY9146.

AWW10151 is the final intermediate in the renaturation of a recombinant protein to AAW22901, which is an active anti-obesity protein for the regulation of fatty tissue and treatment of obesity related diseases, c.g. diabetes, cardiovascular disease and cancer. The production of AAW22901 via AAW10151 provides a high yield of active protein, and permits large scale manufacture with a high concentration of protein curing the folding stage. AAW10151 already has the correct tertiary structure and conversion to AAW22901 is almost quantitative, with minimal formation of S-S linked dimers or multimers, negating the need for an aggregation preventing agent. AAW10151 is stable in the presence or absence of denaturant, is soluble in phosphate buffered saline and can be purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
/note= "free Cys residue or part of mixed disulfide with, e.g. Cys, glutathione or 2-mercaptoethanol when Cys146 is free Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                      /note= "free Cys residue or part of mixed disulfide with, e.g. Cys, glutathione or 2-mercaptoethanol when Cys96 is free Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Properly folded intermediate for obesity protein - prepd. from inclusion bodies, provides high yield of active protein for treatment of obesity and its complications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKWDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDPIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biologically active obesity protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22901 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 21; 66pp; English.
                                                                                                                                                                                                                                                                                                                    95US-0000451P.
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                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                          Mackellar W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-087317/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 146 AA;
                                                                      Modified-site
                                                                                                                                                                                                                                                                       20-JUN-1996;
                                                                                                                                                                                                                                                                                                                    22-JUN-1995;
                                                                                                                                                                                 WO9700886-A1
                                                                                                                                                                                                                             09-JAN-1997.
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02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22901;
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                                                                                                                                                                                                                                                                                                                                                                                                          Hale JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the human obesity protein. It can be used in the formulation of the invention. The formulation of the invention is a soluble parenteral formulation that comprises an obesity protein and a preservative selected from an alkylparaben, chlorobutanol, or a mixture. The compositions can be used for treating obesity and disorders associated with obesity. In the formulations, the obesity protein remains stable and soluble at much higher concentrations and at a pH range acceptable for a soluble, parenteral formulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intermediate, recombinant, production, obesity, regulation, fatty tissue, treatment, disease, diabetes, cardiovascular, cancer, properly folded.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                           New obesity protein compositions - comprising a soluble parenteral formulation containing a preservative selected from an alkyl:paraben and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "R3 is absent, Met, Met-R4 or leader sequence (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94), and R4 is any amino acid other than Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPIQKVQDDTKTLIKTLVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLLTLSKMDQTLAV
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 736; DB 2; Length 146; 100.0%; Pred. No. 9e-73; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Properly folded obesity protein intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 6; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW10151 standard; protein; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Val-R3
                                                                                                                                                                                                                                                                       Beals JM, Dodd SW, Pekar AH;
                                                                                                                  97EP-00300299
                                                                                                                                                            96US-0010229P
96GB-00002408
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 146; Conservative
                                                                                                                                                                                                                           (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                 NPI; 1997-365736/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        chloro:butanol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                  17-JAN-1997;
                                                                                                                                                            19-JAN-1996;
07-FEB-1996;
                         EP784979-A2
                                                                      23-JUL-1997
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02-OCT-1997
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Location/Qualifiers

(first entry)

97WO-US001188 96US-0011238P

& CO BLI

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New compound comprising obesity protein and divalent metal cation - for treatment of obesity and associated conditions, required at lower dose
                                                                                                                   Obesity protein; diabetes; cancer; cardiovascular disease;
divalent metal cation; leader sequence.
                                                                                Obesity protein complexed with a divalent metal cation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 26; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-415077/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    than free protein.
                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIL ) LILLY
                                                                                                                                                                                                                                                                                                                                                                           24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1996;
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                            WO9728824-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffmann JA;
                                       12-MAR-1998
                                                                                                                                                                                                                                                                                                                                   14-AUG-1997.
AAW30791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW26194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW10151 is a properly folded intermediate for the production of the biologically active obesity protein AAW22901, which has a similar biologically active obesity protein AAW22901, which has a similar structure but comprises a disulphide bridge between (9996 and Cys146.

AAW10151 is the final intermediate in the renaturation of a recombinant protein to AAW22901, which is an active anti-obesity protein for the protein to fatty tissue and treatment of obesity related diseases, e.g. diabetes, cardiovascular disease and cancer. The production of AAW22901 via AAW10151 provides a high yield of active protein, and permits large scale manufacture with a high concentration of protein germits large scale manufacture with a high concentration of protein curing the folding stage. AAW10151 already has the correct tertiary structure and conversion to AAW22901 is almost quantitative, with minimal formation of S-S linked dimers or multimers, negating the need for an aggregation preventing agent. AAW10151 is stable in the presence or absence of denaturant, is soluble in phosphate buffered saline and can be purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLSTLDSLGGVLEASGYS 120
                     Intermediate, recombinant, production, obesity, regulation, fatty tissue, treatment, disease, diabetes, cardiovascular, cancer, properly folded.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Properly folded intermediate for obesity protein - prepd. from inclusion bodies, provides high yield of active protein for treatment of obesity and its complications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VPIQKVQDDTKTLIKTIVTKINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                           /note= "R3 is absent, Met, Met-R4 or leader sequence (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94), and R4 is any amino acid other than Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 736; DB 2;
100.0%; Pred. No. 9e-73;
tive 0; Mismatches 0;
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                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 21; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                   96WO-US010613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mackellar W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-087317/08.
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                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-1996;
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The present sequence represents a human obesity protein, which is complexed with a divalent metal cation e.g. zinc and optionally has a leader sequence. It is used to treat obesity and conditions (particularly type II diabetes, cardiovascular disease and cancer) associated with it. When formulated with the metal ion, it is more active, allowing reduction in dose and thus reduction in cost and toxic side effects
                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obesity protein analogue; divalent metal cation complex; therapy; cancer; obesity; obesity associated disorder; diabetes; cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                       2; Length 146;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                       100.0%; Score 736; DB 2; 100.0%; Pred. No. 9e-73;
                                                                                                                                                                                                                                                   0; Mismatches
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nes 146; Conserv
                                                                                                                                                                Sequence 146 AA;
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AAW30791 standard; protein; 146 AA

AAW30791 ID AAW3 XX RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW26189, AAW26190 and AAW26192-W26201 represent obesity protein analogues contained in the compound of the invention. These sequences were synthetically created from the sequence shown in AAW26191. The compound of the invention comprises one of these obesity protein analogues complexed with a divalent metal cation (preferably Zn++). The specification does not indicate where the divalent metal cation complexes to on the obesity protein analogue. The compound of the invention (or a parenteral pharmaceutical formulation containing it) can be used to treat obesity. It may also be used to treat disorders associated with obesity such as diabetes, cardiovascular disease and cancer. The compound allows effective pharmacological treatment at lower doses that significantly because the misus of toxic or other undesirable effects. In addition, because the amount of protein administered is less, the cost of the unit dosage form to the patient is reduced
                                                                                                                                  /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
Thr or Val"
                                                                                                                                                                                                                                                                                                                                            /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
                                                           'note= "optionally replaced with Gln, Asn, Ala, Gly, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obesity protein analogue complexed with divalent metal cation - useful for treating obesity and associated disorders, e.g. diabetes, cardiovascular disease and cancer.
                                                                                              /note= "optionally replaced with Ala, Glu, Asp, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
                                                                                                                                                                                                                                              Ser"
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                                                                                                                                                                                                                                              'note= "optionally replaced with Lys or
                                                                                                                                                                                                                                                                                            replaced with Glu"
                                                                                                                                                                                             /note= "optionally replaced with Ala"
                                                                                                                                                                                                                                                                      'note= "optionally replaced with Pro"
                                                                                                                                                                     'note= "optionally replaced with Arg"
                                                                                                                                                                                                                                                                                                                    'note= "optionally replaced with Asp"
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100.0%; Pred. No. 9e-73;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                       replaced
                        Location/Qualifiers
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                                   96. .146
                                                                        Pro"
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                                                                                  Misc-difference
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                                                Misc-difference
                                   Disulfide-bond
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Synthetic.
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YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                           TEVVALSRLQGSLQDMLWQLDLSPGC 146
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                                                               TEVVALSRLQGSLQDMLWQLDLSPGC
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                                                                                                                                                                                                                                    AAW34483 standard; protein; 146
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Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                Human obesity protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Conservative

Local Similarity

Matches 146;

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Gaps

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Indels

AAW32575;

RESULT 11 AAW3257

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/note= "optionally replaced with Gln, Asn, Ala, Gly, Ser,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally replaced with Ser, Asn, Gly, His, thr, or Val"
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                                                                                                                                                                                                                                                                                                                                         Obesity protein analogue; obesity associated disorder; therapy.
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Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "optionally replaced with Ala"
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                                                                                 TEVVALSRIQGSIQDMLWQLDLSPGC 146
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                                                                                                                                                                                            AAW34489 standard; protein; 146 AA
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96GB-00002409.
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07-FEB-1996;
                                                                                                                                                                                                                                                                    17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP784982-A2
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                 AAW34489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an anti obesity protein analogue used in the treatment or prevention of a condition associated with an excess of neuropeptide Y. The protein analogue is useful in the treatment or prevention of disorders or diseases pertaining to the heart, blood vessels or the renal system, conditions related to increased sympathetic nerve activity, cerebral diseases and diseases related to the central nerve activity, cerebral diseases and diseases related to the central celated to abnormal gastrointestinal motility and secretion, diseases related to abnormal gastrointestinal motility and secretion, abnormal district and food intake disorders, diseases related to sexual dysfunction and reproductive disorders, and conditions or disorders associated with obesity. The protein analogue has improved properties due to its lower isoelectric points and due to specific substitutions to the human obesity protein, and is therefore superior therapeutic agents. It is more readily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                          Anti obesity protein analogue; neuropeptide Y; radiovascular; renal; cerebral; central nervous system; CMS; heart; blood vessel; sympathetic nerve; mouse; human; pain; nociception; abnormal gastrointestinal motility; secretion; abnormal drink intake disorder; abnormal food intake disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New use of biologically active anti-obesity protein analogues - for treating conditions associated with excess neuropeptide Y, e.g. cardiovascular, renal, cerebral or CNS disorders.
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100.0%; Pred. No. 9e-73;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tinsley FC;
                                                                                                                                                                                                                                                                       abnormal drink intake disorder; abnormal roum mucasexual dysfunction; reproductive disorder; obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephens TW,
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
96. .146
                                            AAW32575 standard; protein; 146 AA.
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95US-0000752P.
95US-0005910P.
95US-0005911P.
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                                                                                                                                                           Anti obesity protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96EP-00304723
                                                                                                                      (first entry)
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Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1995;
27-OCT-1995;
27-OCT-1995;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1996;
                                                                                                                      22-JAN-1998
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Asp, Leu"

Pro,

Asp, Asn, Met, Leu"

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61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

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                                                                                                                                                                         1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Ala can be replaced with Ser, Asn, Gly, His, Pro,
 preservatives is reduced. At pH above 8.0, obesity proteins remain in solution in the presence of certain preservatives, making possible a multi-use parenteral formulation containing those preservatives
                                                                                                                                                       1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDPIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; obesity protein; soluble; parenteral formulation; anionic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asp,
Leu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "His can be replaced with Gln, Asn, Ala,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ser"
                                                                                             Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Trp can be replaced with Ala, Glu,
ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Trp can be replaced with Ala, Glu, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or pharmaceutically acceptable salt thereof"
                                                                                        100.0%; Score 736; DB 2; Length 1
100.0%; Pred. No. 9e-73;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Asp can be replaced with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Gly can be replaced with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Leu can be replaced with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Ser can be replaced with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obesity protein analogue formula II SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Gly can be replaced
                                                                                                                                                                                                                                                                                                TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                TEVVALSRIQGSIQDMLWQLDLSPGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; Ob protein.
                                                                                                                                                                                                                                                                                                                                                                                   AAW53342 standard; protein; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-00306420
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                           Local Similarity 100.
ses 146; Conservative
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                                                               Sequence 146 AA;
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ID AAW5
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              and a preservative selected from an alkyparaben, chlorobutanol, or a mixture. The compositions can be used for the treatment of obesity and disorders associated with obesity. In the formulations, the obesity protein analogue remains stable and soluble at much higher concentrations and at a pH range acceptable for a soluble, multi-use parenteral formulation
                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of human obesity protein. The invention discloses a storage-stable, soluble formulation comprising an obesity protein and a preservative, and having a pH greater than 8.0. The obesity protein used in the formulation is preferably bio-synthesised in a host cell transformed with a recombinant DNA comprising a synthetic or semisynthetic DNA encoding tge protein. The soluble formulation can be administered to mammals to treat obesity (claimed), especially humans when the obesity protein is human obesity protein. It was found that the physical stability of obesity proteins in the presence of preservatives such as phenol and cresol changes abruptly and is greatly enhanced at pH values above 8.0, such that the aggregation of obesity proteins caused by
                                                                                                                                                                                                                                                                                              YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obesity protein soluble formulation for treating obesity - has pH greater than 8.0, at which aggregation of obesity proteins by preservatives is reduced allowing production of multi-use formulation.
parenteral formulation that comprises an obesity protein analogue
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                                                                                                                                                                                                                                   1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                      Length 146;
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                                                                                                                                                    100.0%; Score 736; DB 2; 100.0%; Pred. No. 9e-73;
                                                                                                                                                                                    Mismatches
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97US-0054886P.
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                                                                                                                                                                                    Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                         Sequence 146 AA;
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                                                                                                                                                                                  Matches 146;
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(TSUJ/) TSUJI M.
(MATS/) MATSUMIYA T.
                                   WPI; 1999-629222/54.
                                                                                                                                                                                                                                                          Similarity
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Matches 146;
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                                                                                                                                                                           producing obesity protein analogues for use in the present invention as part of a soluble parenteral formulation. The soluble parenteral formulations comprises an obesity protein or obesity protein analogue and an anionic amphiphilic compound. The formulations are used for treating a concentration of 15-50 mg/ml. The proteins are preferably present at a concentration of 5-50 mg/ml. The anionic amphiphilic compound solubilises and stabilises the protein
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                                                                                                       Parenteral obesity protein formulations - containing anionic amphiphilic solubiliser and stabilise.
                                                                                                                                                                represents an obesity protein generic formula for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leptin; brain function improver; brain denaturation disease; therapy; Alzheimer's disease; old age dementia; Pick's disease; hereditary abhasia; Huntington's chorea; Parkinson's disease; progressive subcutaneous gliosis; progressive supranuclear paralysis; thalamus denaturation; myoclonus epilepsy.
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                                                                                                                                                                                                                                                                                              100.0%; Score 736; DB 2; Length 146; 100.0%; Pred. No. 9e-73; ative 0; Mismatches 0; Indels
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                                                                                                                                            Disclosure; Page 9; 45pp; English.
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  96US-0024121P
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                                    (ELIL ) LILLY & CO ELI.
                                                          Beals JM, Rinella JV;
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SHIRAISHI T.
SASAKI K.
TAKEDA H.
                                                                                 WPI; 1998-180894/17.
                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                         Seguence 146 AA;
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 23-AUG-1996;
23-AUG-1996;
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YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                   This sequence represents human leptin. The invention relates to a brain
                                                                                                                                                                                                                       function improver containing mammalian leptin as the active component. The brain function improver is useful as a treating agent for brain denaturation diseases such as Alzheimer's disease, old age dementia, pick's disease, Huntington's chorea, Parkinson's disease, Parkinson syndrome, progressive subcutaneous gliosis, progressive subcutaneous gliosis, progressive subcutaneous gliosis, progressive subcanuclear paralysis, thalamus denaturation, hereditary aphasia and myoclonus epilepsy, and other diseases causing deterioration of brain function
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A brain function improver - useful for treating brain disorientation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 736; DB 2; Length 1
100.0%; Pred. No. 9e-73;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEVVALSRLOGSLODMLWQLDLSPGC 146
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                                                                                                                         Disclosure; Page 5; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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using sw model OM protein - protein search,

(without alignments) 509.074 Million cell updates/sec May 4, 2006, 21:50:51; Search time 27.5945 Seconds Run on:

US-10-623-189-1 736 1 VPIQKVQDDTKTLIKTIVTR......SRLQGSLQDMLWQLDLSPGC 146

Title: Perfect score: Sequence:

283416 seqs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir2:* 4: pir4:* PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description					rat ob - rat	glutamate dehydrog	hypothetical prote	probable myosin he	hypothetical prote	sensory transducti	probable soluble l	phosphotransferase	ribosomal protein	carbamoyl-phosphat	probable trehalose	hypothetical prote	hypothetical prote	acriflavine resist	hypothetical prote	probable membrane	hypothetical prote	5,10-methylenetetr	glutamate-1-semial	beta transducin-li	hypothetical prote	probable membrane	prolactin, 20K - M	prolactin II precu	exopolysaccharide
SUMMAKIES	ΩI	LTHU	153166	LTMS	LTRT	155622	AB3281	S54039	T01362	H84583	S75514	A10055	B42374	S77486	A83967	E86305	B89954	T46011	D70117	T26551	S59792	C72430	D70424	E81358	S76414	AB2202	S46092	A28106	B32477	AB2959
	90	1	7	H	н	N	C4	0	~	0	7	8	7	7	7	0	N	0	7	~	~	~	7	0	7	N	N	0	~	~
	Query Match Length DB	167	166	167	167	167	1600	444	829	952	420	639	574	173	362	822	409	570	1036	403	1438	142	296	424	1191	559	674	177	200	421
*	Query Match	100.0	97.9	84.1	82.2	82.2	11.1	10.9	10.7	10.7	10.6	10.6	10.5	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.1	10.1	10.1	10.1	10.1
	Score	736	720.5	619	605	605	81.5	80.5	79	79	78	78	77.5	76.5	76.5	76.5	92	16	76	75.5	75.5	75	75	75	75	74.5	74.5	74	74	74
	Result No.		2	ო	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	. 22	23	24	25	26	- 27	28	29

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exopolygaccharide alkaline phosphata kinesin family pro	probable methyl-ac hypothetical prote conserved hypothet	ATP-dependent RNA type III secretion hypothetical prote	phenylalanine-tRNA probable yopC/gen probable membrane	hypochetical prote keratin 20, type I 14-nm filament pro hypothetical prote
D98324 C69676 A56921	H71317 S46754 G82638	D88511 D81746 S44912	H71509 F71486 AC0045	T47924 S37780 JC5625 B84900
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423 462 1695	1228 186	296 672 696	790 921 1119	406 424 462 550
10.1	0.01	0 0 0 0 0	თ თ თ თ თ თ	0 0 0 0 0 0 0 0
4 4 4 4	73.5 73.5 73	73 73	73 73	72.5 72.5 72.5
30 31	3 3 3 3 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	3 3 3 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	39 41 41	4 4 4 4 2 6 4 2

ALIGNMENTS

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Linnu

Williams to see a protein; obesity factor

C. Species: Homo sapiens (man)

C. Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C. Species: Homo sapiens (man)

C. Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C. Accession: Alsysoly (man)

R. Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.

R. Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.

R. Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.

A.; Accession: Alsysolate (man)

A.; Accession: Alsysolate (man)

A.; Accession: Alsysolate (man)

A.; Accession: JE0148

A.; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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100.0%; Score 716; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e-59;
Matches 146; Conservative 0; Mismatches 0; Indels (
RESULT 1
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9 81

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Cipecies: Rattus norvegicus (Norway rat)
Cipate: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
Cipate: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
Cipatession: PC4034; JC4142
Cipatession: PC4034; JC4142
Rightnahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A;Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial
A;Reference number: PC4034
A;Accession: PC4034
A;Accession: PC4034
A;Residues: 1-167 <FUN>
A;Residues: 1-167 <FUN>
A;Cross-references: UNIPROT:PS0596; UNIPARC:UPI0000038DAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: liver C; Comment: This protein is proposed to function as part of a signalling pathway from ad C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rat ob - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 155622
R;Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; T;
J. Clin. Invest. 96, 1647-1652, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross_references: UNIPARC: UP10000038DAF; DDBJ: D49653; NID: 9995614; PIDN: BAA08529.1; P
                                                                                         YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                       61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVTGLDFIPGLHPILSLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VPIHKVQDDTKTLIKTIVTRINDISHTQSVSARQRVTGLDFIPGLHPILSLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Experimental source: adipose tissue
A,Note: The authors translated the codon AAA for residue 32 as Thr
R,Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A,Title: Cloning of rat obese cDNA and its expression in obese rats.
A,Reference number: JC4142; MUID:95251725; PMID:7733988
A,Reference number: JC4142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfaction:
C.Superfaction:
C.Keywords: adipose tissue
C.Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>F:22-167/Product: leptin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                              leptin precursor - rat
N;Alternate names: obese protein; obesity factor
                                                                                                                                                                                                                                                    142 TEVVALSRLQGSLQDILQQLDVSPEC 167
                                                                                                                                                                                                                   TEVVALSRLQGSLQDMLWQLDLSPGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <MUR>
                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leptin precursor - mouse
NyAlternate names: obese protein
Sisternate names: obese protein
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Richang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: Jrf7 < ZEIAA
A;Cross-references: UNIPROT:P41160; UNIPARC:UPI0000003FAA; EMBL:U18812; NID:9746416; PID
C;Superfamily: leptin
C;Superfamily: signal sequence #status rrand;
F;2-2-167/Produint: signal sequence #status rrand;
                                                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: 153166; G0328
R;Mauuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Ta Diabetes 44, 855-858, 1995
Diabetes 44, 855-858, 1995
A;Title: Human Obese gene expression. Adipocyte-specific expression and regional differe A;Reference number: I53166; MUID:95309556; PMID:7789654
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-166 <RES>
A; Cross-references: UNIPROT:P41159; UNIPARC:UP1000014D164; GB:D49487; NID:g904211; PIDN:
Rychehab, F. F.; Lim, M.E.
Submitted to the EMBL Data Library, December 1995
A; Reference number: H01063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-166 <CHE>
A;Cesidues: 1-166 <CHE>
C;Genetics: UNIPARC:UPI000014D164; EMBL:U43415; NID:g1163105; PIDN:AAC31660.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 720.5; DB 2;
Pred. No. 4e-58;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GDB:136420; OMIM:164160
A,Map position: 7q32.1-7q32.1
A,Introns: 48/3
C,Superfamily: leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.3%;
Matches 145; Conservative 0
                          leptin precursor - human
N;Alternate names: obese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: LEP; OB; OBS
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UNIPARC: UPI000013281A; EMBL: Z49209; NID: 9798897; PI
                                                                                                                                        A;Residues: 1-444 < HUN>
A;Cross-references: UNIPROT:Q12355; UNIPARC:UPIOC
B; Exandt, P.; Otto, B.; Ramlow, S.; Blocker, H.
submitted to the EMBL Data Library, January 1995
A;Reference number: S58832
A;Recession: S58835
RiHunt, S.; Bowman, S.; Harris, D.
submitted to the EWBL Data Library, May 1995
A;Reference number: 854031
A;Accession: 854039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 KIGGLDNLTTIGGTLEVVGNFTSL 309
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-829 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: SGD:S0002462
A,Map position: 4R
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                                                                                                                        A; Molecule type: DNA
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Matches
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, j. Mazur, M.; Golteman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443.448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitems A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Accession: AB3281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1600 «KUR»
A;Residues: 1-1600 «KUR»
A;Residues: 1-1600 «KUR»
A;Experimental source: strain 16M
A;Experimental source: strain 16M
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N;Alternate names: hypothetical protein D4214; hypothetical protein YBRB444; hypothetica
N;Alternate names: Byothetical protein D4214; hypothetical protein YBRB444; hypothetica
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 05-Oct-2004
C;Accession: S54039; S58835; $61744; S67871
             A;Title: Molecular cloning of rat obese cDNA and augmented gene expression in geneticall A;Reference number: I55622; MUID:95386724; PMID:7657834
A;Accession: I55622
                                                                                                                                                                      PIL
                                                                A;Accession: IS5622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-167 < RES>
A;Cross-references: UNIPARC:UPI0000038DAF; GB:D45862; NID:g1018990; PIDN:BAA08296.1;
C;Superfamily: leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               juramate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYSTEVVA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 YQQILTSLPSQNVLQIAHDLENLRDLLHLLAPSKSCSLPQTRGLQKPESLDGVLEASLYS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOOILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                  22 VPIHKVQDDTKTLIKTIVTRINDISHTQSVSARQRVTGLDFIPGLHPILSLSKMDQTLAV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQIL 65
                                                                                                                                                                                                                                                                                                                                                     1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                       Length 167;
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                                                                                                                                                                                                                                                                                                    11, Indels
                                                                                                                                                                                                                                                 Query Match 82.2%; Score 605; DB 2; Best Local Similarity 83.6%; Pred. No. 1.2e-47; Matches 122; Conservative 13; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: glutamate dehydrogenase, Ml14104 type
C;Keywords: oxidoreductase
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24.6%; Pred. No. 54;
:ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 TEVVALSRLQGSLQDILQQLDLSPEC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVVALSRLQGSLQDMLWQLDLSPGC 146
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Best Local Similarity 24.6%
Matches 32; Conservative
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A;Molecule type: DNA
A;Residues: 1-44 <ARDA.
A;Residues: 1-44 <ARDA.
A;Residues: 1-44 deRDA.
A;Cross-references: UNIPARC:UPI000011281A; EMBL:X84162; NID:9706817; PIDN:CAA58971.1; P
R;Brandt, P.; Ramlow, S.; Otto, B.; Bloecker, H.
R;Brandt, P.; R5-90, 1996
A;Est 12, 85-90, 1996
A;Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacchar
A;Reference number: S61741; MUID:96381250; PMID:8789263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.M.; Kai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-444 <BLO>
A;Cross-references: UNIPARC:UP1000013281A; EMBL:274351; NID:g1431498; PIDN:CAA98873.1;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-444 <BRW>
A;Residues: 1-444 <BRW>
A;Cross-references: UNIPARC:UPI000013281A; EMBL:X84162; NID:9706817; PIDN:CAAS8971.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
B;Bloecker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable myosin heavy chain At2g14730 - Arabidopsis thaliana
NiAlternate names: hypothetical protein T29F13.6
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: T01362; C84760
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the BMBL Data Library, May 1998
A; Poscription: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PVETVSDSLOFSFNGNOTKITPDDLVWANNISLTDVHSVSPANLOKINSSLGPINNSISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: protoplast secreted protein 1 precursor C;Keywords: transmembrane protein R;5-21/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 10.9%; Score 80.5; D. Local Similarity 24.3%; Pred, No. 13; hes 35; Conservative 23; Mismatches
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 875514
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P74004; UNIPARC:UPI00000D3509; EMBL:D90911; GB:AB001339; NI:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon: GTG
S,Superfamily: sensory transduction system regulatory protein; response regulator homol.
C;Keywords: phosphoprotein
F;33.-146/Domain: response regulator homology <RRH>
F;33.-146/Domain: response regulator homology <RRH>
F;85/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 LLDLTLPDSQGLNSLPKLQSHPQNLPITVLTHYQDEBLALEAVRQGAQDYLVKRDVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SCHLPWASGLETLDSLGG-----VLEASGYSTEVVALSRLQGSLQDMLWQLDLS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 PGLHPILTLSKMDQTLA---VYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSK----
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                                                                                                                                                                                                                                                                A;Accession: $75514
A;Status: nucleic acid sequence not shown, translation not shown
A;Molecule type: DM
A;Residues: 1-420 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.6%; Score 78; DB 2; Length 420; 28.2%; Pred. No. 21;
                                                                                                                                                                                                                                     A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.6%; Score 78; ub.
Best Local Similarity 28.2%; Pred. No. 21;
Matches 33; Conservative 18; Mismatches
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C;Superfamily: soluble lytic transglycosylase
C;Keywords: glycosidase; hydrolase
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Matches 32; Conserva
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C;Genetics:
A;Gene: At2g20010
A;Map position: 2
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: C84760
A; Accession: C84760
A; Accession: C84760
A; Residues: J-829 < GTO>
A; Residues: J-829 < GTO>
A; Coque-references: UNIPARC:UPI000004A13E; GB:AE002093; NID:g3132472; PIDN:AACI6261.1; GCGGERERCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2g20010 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84583
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
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N;Alternate names: protein slr1324
C;Species: Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 VGSEENESSESRLIHDELTQGSSSSLKKKARKQLLMLVEELTNLREYIHIN----- 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 LHPILTLSKMDQTLAVYQQILTSMPSR--NVIQISNDLENLRDLLHVLAF-----SK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDML 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.7%; Score 79; DB;
Best Local Similarity 21.5%; Pred. No. 40;
Matches 34; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               A,Gene: At2g34730; T29F13.6
A,Map position: 2
A,Introns: 728/2; 770/3
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-952 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
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22;

44; Indels

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probable soluble lytic murein transglycosylase (EC 3.2.1.-) [imported] - Yersinia pesti.
                                  C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: A10055
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davie, P.; Dougan, G.; il, M.; Stutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Title: Genome sequence of Yersinia pestis, pMID:11586360
A; Accession: A10055
A; Status: preliminary
A; Status: preliminary
A; Status: DNA
A; Residues: L-639 - KUR>
A; Cross-references: UNIPROT: QBZIP2; UNIPARC: UPI00000CD6CB; GB:AL590842; PIDN:CAC89308.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 TOSVSSKOKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 LHVLAFSKSCHLP------WASGLETL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
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carbamoyl-phosphate synthetase (glutaminase subunit) pyrAA [imported] - Bacillus halodu C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: A83967
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83567, MUID:20512582; PMID:11058132
A;Accession: A83967
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-362 <STO>
A;Cross-references: UNIPROT:Q9K8V8; UNIPARC:UPI0000126F32; GB:AP001515; GB:BA000004; NI A;Residues: pyrAA
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-822 <STO>
A;Cross-references: UNIPROT:Q9FZ57; UNIPARC:UPI0000A0CF7; GB:AE005172; NID:g9802765; :
C;Genetics:
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                                                                                                                                         70 VADGKKQLIEVPLTKSNSITHITNGVSGAKVVVRPAAPGTGVIAGGAVRTVLBLAGVKN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 DDFESMNPAIHGLIVKEACDIPSNWRSB-ESLDSLLKAKQIPGLSGIDTRKLTRLIRMHG 124
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Length 173;
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                                                         41; Indels
                                                                                                            6 VQDDTKTLIKTIVTRINDISH-TQSVSSKQKVTGLDFIPG
  DB 2;
                                                                                                                                                                                                                                                        10.4%; Score 76.5; DE ilarity 31.2%; Pred. No. 9.2; Conservative 12; Mismatches
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Pred. No. 66;
                                                                                                                                                                                                                      57 TLAVYOQILTSMPSRNVIQISNDLENLRDLLHV
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31.6%;
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125 TLKGQLCPLDV 135
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Best Local Similarity
  Query Match
Best Local Similarity
Matches 29; Conserv
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Matches
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                                                                          phosphotransferase system enzyme I (EC 2.7.3.9) - Staphylococcus carnosus C; Species: Staphylococcus carnosus C; Species: O-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004 C; Accession: B423.4; S17075 B; Kohlbrecher, D.; Eisermann, R.; Hengstenberg, W. J. Bacteriol. 174, 2208-2214, 1992 A; Affitle: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: molecul studies of the gene product.
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NyAlternate names: protein s111812
C;Species: Symechocystis sp.
A;Variety PCC 6803
C;Species: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S77486
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-173 <KANA.
A,Residues: 1-173 <KANA.
A,CTOSS-references: UNIPROT:P73304; UNIPARC:UPI000013507A; EMBL:D90905; GB:AB001339; NIC
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000017007F; EMBL:X60766; NID:g46907; PIDN:CAA43176.1; PID C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I hc C;Keywords: phosphoprotein; phosphotransferase; sugar transport system F;5-563/Domain: phosphotransferase system enzyme I homology <PT1>
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-574 <KOH>
A;Residues: 1-574 <KOH>
A;Cross-references: UNIPROT:P23533; UNIPARC:UPI000013287C; GB:M69050; NID:g153073; PIDN:A;Cross-references: UNIPROT:P23533; UNIPARC:UPI00013287C; GB:M698tenberg, W.
Bur: J. Biochem. 197, 9-14, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system. Purifid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 KTLIKTIVTR---INDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 MPSRNVIQISNDLENIRDLIHVLAFSKSCHLPWASGLETLDSLGGVLE--ASG---YSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 77.5; DB 1; Length 574;
25.0%; Pred. No. 34;
tive 27; Mismatches 54; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equencing of the ptsH gene.
A;Reference number: S15367; MUID:91200066; PMID:1901791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: rps5
C;Superfamily: ribosomal protein S5/S2
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.0%
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-90 <EIS>
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ò.	DOTLA	
QQ	470 GLDFMSELNGIIPESEMQMRKIPLQLPEQDVIQQYSQSNNRLIILGFFGTLA 521	
è	98 LPWASGLETLDSLGGVLEASGYSTEVVALSR 128	
Q	522 EPWNSGTKEMDLKLINPELKGTLKALCNDPKTTVVVLSR 559	

Search completed: May 4, 2006, 22:03:30 Job time : 28.5945 secs

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bubalus bub
                                                    alopex lago
vulpes vulp
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canis famil
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phoca vitul
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camelus dro
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
13-EEP-2005 (Rel. 48, Last amnotation update)
Leptin precursor (Obesity factor) (Obese protein).
Name-LEP; Synonyms-OB;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE-95075453; PLUMEd=7984236; DOI=10.1038/37242580;
ABDLINE-95075453; PLUMEDENCE., Maffei M., Barone M., Leopold L., Friedman J.M.;
"Positional cloning of the mouse obese gene and its human homologue.";
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MEDILIBE-953095556; Pubmed=7789654;
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Medicaki H., Ogawa Y., Isbe N., Sacoh N., Okazaki T., Shigemoto
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
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Q861R2_BUBBU
Q86KS6_ALOLA
Q8MKS9_VULVU
Q8MKS_PWILVU
Q8MK61_CANFA
QBMK61_CANFA
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J. Biol. Chem. 270:27728-27733(1995)
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Nature 374:479-479(1995).
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 TISSUE-Placenta, Lance Scale March.

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REDLINE=22388257; PubMed=12477922; DOI=10.1073/pnas.242603899;

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                                                                                                 Diabetes 45:675-678(1996)
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Tobesity.";

Nat. Genet. 18:213-215(1998).

Lost Genet. 18:213-215(1998).

Control May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constrancy of the adipose mass.

Constrainty Interacts with SIGLECG.

SUBCELLULAR LOCATION: Secreted.

Constrainty Defension LEP may be a cause of autosomal recessive obesity [MIM:601665].

Constrainty: Belongs to the leptin family.

CC -: SIMILARITY: Belongs to the leptin family.

CC -: DATABASE: NAME-RED Systems con/asp/gitebuilder.asp?bodyId=213".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                   VARIANT MORBID OBESITY TRP-105.
MEDILIRE-98160176; PubMed=9500540;
Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;
"A leptin missense mutation associated with hypogonadism and morbid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_004196.

V -> M (in dbSRP:17151919).

/FTId=VAR_004197.

R -> W (in morbid obesity and hypogonadism).

/FTId=VAR_008094.

V -> M (in dbSNP:1800564).

/FTId=VAR_011995.

Q -> R (in Ref. 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
3D-structure; Diabetes mellitus; Disease mutation; Obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in 30% the clones)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005612; P:energy reserve metabolism; TAS.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Bartholomew D.W., McClellan J.M.; "A novel polymorphism in the leptin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF008123; AAB63507.1; -; mRNA.—
EMBL; AY996373; AAX81413.1; -; Genomic_DNA.
EMBL; BC060830; AAH60830.1; -; mRNA.
EMBL; BC069452; AAH69452.1; -; mRNA.
EMBL; BC069527; AAH69527.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U18915; AAA60470.1; -; mRNA.

EMBL, D49487; BAA08448.1; -; mRNA.

EMBL, U43653; AAC50400.1; -; mRNA.

EMBL, U4315; AAC31660.1; -; Genomic_DNA.

EMBL, D63710; EAA09830.1; -; Genomic_DNA.

EMBL, D63519; BAA09830.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1AX8; X-ray; @=22-167.
Ensembl; ENSG00000174697; Homo sapiens.
HGNC; HGNC: 5553; LEP.
MIM; 164160; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leptin.
                                                      Hum. Mutat. 12:220-220(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
167
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PIR; I53166; I53166.
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25
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NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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002750;
                                                                                                                                                 61
                                                                 SEQUENCE
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                                                                                    61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                  141
                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                    nouso parteus incumani.
Eukaryota, Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                             82 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLBASGYS
                                                     1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                     Gaps
                                     .;
0
                      Length 167;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted (By similarity). EMBL; BC069323; AAH69323.1; -; mRNA. HSSP; P41159; 1AX8. SMR; QGNTS8; 24-167.
                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                       ö
                      Score 736; DB 1;
Pred. No. 9.1e-60;
                                     0; Mismatches
                                                                                                                                                                         167
                                                                                                                            142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
                                                                                                                   121 TEVVALSRIQGSIQDMLWQLDLSPGC 146
                                                                                                                                                                        PRT;
                       100.0%;
                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rescued clones;
                                                                                                                                                                        QGNTS8 HUMAN PRELIMINARY;
QGNTS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
                                       Conservative
                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
72
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                      Matches 146;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X., Sockey P.K., Rosteck P.R., Rosteck P.R., "Cloning of Obese genes from different species: a comparison of gene structures and the sequences of the obese gene products,
                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                               Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                             PRINTS; PRO0495; LEPTIN.
ProDom; PD005699; Leptin; 1.
SEQUENCE 167 AA; 18613 MW; BEIA046FFB1554DB CRC64;
                                                                                                                                                                                                                                                                                                                                  ; Score 736; DB 2;
; Pred. No. 9.1e-60;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                   GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0007165; P:aignal transduction; IEA.
InterPro; IPR012351; Cytokine_4_hix.
InterPro; IPR00065; Leptin.
PF020024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEVVALSRLQGSLQDMLWQLDLSPGC 167
Ensembl; ENSG0000174697; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR01351; Cytokine_4_hlx.
InterPro; IPR01055; Leptin.
PANTHER; PTH711724; Leptin; 1.
PEm; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
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HSSP; P41159; 1AX8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=LEP; Synonyms=OB;
Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMR; 002750; 3-146
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61
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                     leptin.",
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                                                                                                                                                                YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                        120
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                                                                                                              1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D.P., Zhang X., Haining H.M.;
"Goxilla leptin genomic sequence.";
"Goxilla leptin genomic sequence.";
"Goxilla leptin genomic sequence.";
"Covilla leptin genomic sequence.";
"Covilla leptin genomic sequence.";
-!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of IEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                     Gorilla gorilla gorilla (Lowland gorilla).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;

Gorilla.

MCBI_TAXID=9595;
                                                                                                                             1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                              61 YQQILTSMPSRNMIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYS
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.9%; Score 728; DB 1; Length 146; 98.6%; Pred. No. 4.2e-59; Live 2; Mismatches 0; Indels
                                                              Length 146;
                                                                                       Indels
                          By similarity.
02C42A06B554D55C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / similarity.
02C43BF6B9A4C85C CRC64;
                                                                                       ö
                                                            99.6%; Score 733; DB 1;
99.3%; Pred. No. 1.5e-59;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULĀR LOCATION: Secreted (Probable). SIMILĀRITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                              01-NNV-1997 (Rel. 35, Created)
01-NNV-1997 (Rel. 35, Last sequence update)
01-NNY-2005 (Rel. 47, Last annotation update)
Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                        146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U72872; AAB17091.1; -; Genomic_DNA.
HSSP; P41159; 1AX8.
                                                                                                                                                                                                                               TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                 TEVVALSRIQGSLODMIWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вy
                                    16059 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA; 16031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD005698; Leptin; 1.
ProDom; PD005698; Leptin; 1.
                                                                         Best Local Similarity 99.3
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.6
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                          146
                                                                                                                                                                                                                                                                                                                                                                                Name=LEP; Synonyms=OB
                        96 1
146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
              Obesity.
DISULFID
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DISULFID
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                                    SEQUENCE
                                                              Query Match
                                                                                                                                                                                                                                                                                                        GORGO
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                       1 VPIQKVQDDTKTLIKTIVTRISDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
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-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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VPIOKVODDTKTLIKTIVTRINDISHTOSVSSKOKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE. Schoner B., Smith D.P., Haiung H.M., Zhang X., Rockey P.K., Rosteck P.R.; Roteck P.R.; Roteck P.R.; Rotioning of obese genes from different species: a comparison of the gene structures and the sequences of the obese gene products,
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; 3F50A13338FFDBD4 CRC64;
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-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OB PONPY STANDARD; PRT; 146 AA. 095234; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-NAY-2005 (Rel. 47, Last annotation update) Leptin (Obesity factor).
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HSSP; P41159; 1AX8.
                                                                                                                                                                                                                                                                                                                  121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                       TEVVALSRLQGSLQDMLWQLDLSPGC 146
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InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam, PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN; 1.
ProDom; PD005698; Leptin; 1.
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16195 MW;
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142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
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Q6T8R8_BUBBU
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      61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDRLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus monkeys. Effects of insulin, body weight, and non-insulin-dependent diabetes mellitus.";
J. Biol. Chem. 271:25327-25331(1996).
-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=LEP; Synonyms=OB; Macaque).
Macaca mulatta (Rhesus macaque).
Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
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MEDLINE-96411743; PubMed-8810296; DOI=10.1074/jbc.271.41.25327;
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By similarity.
E7D9F30628A5BBE9 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
Leptin precursor (Obesity factor).
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                                                                           121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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HSSP; P41159; 1AX8.
SMR; Q28504; 24-167.
Interpro; IPR012351; Cytokine_4_hlx.
Interpro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
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PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                         STANDARD;
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Q28504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
"Molecular cloning of feline leptin cDNA.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gape
                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-may-2005 (Rel. 47, Last annotation update)
10-may-2005 (Rel. 40)
Name=LEP; Synonyms=OB;
Relis silvestris catus (Cat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Relinae; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 86.8%; Score 639; DB 1; Length 16 al Similarity 86.3%; Pred. No. 8.1e-51; 126; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptin.
By similarity.
643720DBB0AB4B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBCELLULAR LOCATION: Secreted (Probable).
SIMILARITY: Belongs to the leptin family.
167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P41159; 1AX8.
SMR; Q9N2C1; 24-167.
InterPro; IPR01251; Cytokine_4_hlx.
InterPro; IPR010365; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB041360; BAA95481.1; -; mRNA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 21 POI
22 167 Leg
117 167 By
167 AA; 18584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Obesity; Signal.
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STANDARD;
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25.4

Market Co

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NUCLEOTIDE SEQUENCE OF 22-167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 1-48
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167
167
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117
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VARIANT
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQILTSLPSRNVVQISNDLENLRDLLHLLAASKSCPLPQVRALESLESLGVVLEASLYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OB BOVIN STANDARD; PRT; 167 AA.
P50595; 097918; 095133; 097829;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 37, Last annotation update)
10-MAY-2005 (Rel. 34, Last annotation update)
10-MAY-2005 (Rel. 34,
                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                            TISSUE=Adipose tissue;
Rajendran S., Shukla D.C., Saravanan B.C.;
"Cloning and sequencing of buffalo leptin gene.";
Submitred (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY427959; AAR05862.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ji S., Spurlock M.E.; "Partial cloning of bovine obesity gene."; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tellam R.L., Briscoe S., Vuocolo A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;
                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.3%; Score 628; DB 2;
87.0%; Pred. No. 7.1e-50;
tive 10; Mismatches 9;
   146 AA.
                                                                                                                                                                                                                                                                                                                                SWR; OGTBRB; 3-146.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; P:hormone activity; IEA.
GO; GO:0001165; P:signal transduction; IEA.
InterPro; IPR000065; Leptin.
PF02024; Leptin.
                                                                                                       Bubalus bubalis (Domestic water buffalo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEVVALSRLQGSLQDMLRQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEVVALSRIQGSLODMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leptin.
                                                                                                                                                          Pecora; Bovidae; Bovinae; Bubalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 22-167.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
CHAIN <1 146
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BUBBU PRELIMINARY;
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                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                   Leptin (Fragment).
                                                                                                                                                                           NCBI_TaxID=89462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
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                     26TBRB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OB BOVIN
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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use as long as its content is in no way modified and this statement is not
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"Exon two of the bovine obese, leptin, gene.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

-I- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liefers S.C.; "Genotype effects of bovine leptin mutations on pre- and postpartum
                                                                                                                                                                                                                              MEDLINE=20063685; PubMed=10594237; DOI=10.1007/s003359901180; Konfortov B.A., Licence V.E., Miller J.R.; "Resequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 60-146.
MEDLINE=96269621; PubMed=8661738; DOI=10.1007/8003359900118;
Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
"Chromosomal localization of the bovine obesity (OBS) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lien S., Sundvold H., Klungland H., Vaege D.I.;
"Two novel polymorphisms in the bovine obesity gene (OBS).";
Anim. Genet. 28:245-245(1997).
TISSUE=White adipose tissue;
Kawakita Y., Abe H., Miyashige T.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leptin concentrations.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                               NUCLEOTIDE SEQUENCE, AND VARIANTS CYS-25 AND VAL-80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AB003143; BAA19750.1; -; mRNA.
EMBL, AJ236854; CAB645255.1; -; Genomic_DNA.
EMBL, AJ246854; CAB3618.1; -; Genomic_DNA.
EMBL, AJ512639; CAD54745.1; -; Genomic_DNA.
EMBL, AJ512639; CAD54745.1; -; Genomic_DNA.
EMBL, AJ512639; CAD54745.1; -; Genomic_DNA.
EMBL, Y11369; CAD572197.1; -; Genomic_DNA.
EMBL, W18833; AAB18762.1; -; Genomic_DNA.
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By similarity.
R -> C.
A -> V.
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HSSP; P41159; 1AX8.
SMR; P50595; 24-167.
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EMBL; U50365; AAB61244.1; -; Genomic_DNA.
EMBL; U65793; AAB06579.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE, AND VARIANT CYS-25.
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InterPro; IPR012551; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
PAM: PR02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005699; Leptin; 1.
Obesity; Polymorphism; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                          Mamm. Genome 10:1142-1145(1999).
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YQQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                           82 YQQILTSLPSRNVVQISNDLENLRDLLHLLAASKSCPLPQVRALBSLESLGVVLEASLYS
                                      VPIQKVQDDTKTLIKTLVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                             22 VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLSLSKMDQTLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McNeel R.L., Mersmann H.J.; andipose tissue regulatory transcript expression in lean versus obese
Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Landrace;
Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides P.G.,
Benkel B.F., McKay R.M., Pelletier G.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";
  ö
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Soares M.A.M., Buclydes R.F., Guimaraes S.E.F., Martins M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=White adipose tissue;
MEDLINE=97009821; PubMed=8856925;
Neuenschwander S., Rettenberger G., Meijerink E., Jorg H.,
  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Meishan;
Dai R., Li N., Hu X., Wu C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
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to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                029406; 019095; Q95251; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NAY-2005 (Rel. 47, Last annotation update) Leptin precursor (Obesity factor).
                                                                                                                                                                                                                                                                                                                                                    167 AA
  10; Mismatches
                                                                                                                                                                                                                                  142 TEVVALSRLQGSLQDMLRQLDLSPGC 167
                                                                                                                                                                                                      121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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    127; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bidwell C.A., Ji S.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramsay T.G., Yan X.;
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1998)
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      Matches
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                                                                                                                                                                                                                                                   YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.",
Anim. Genet. 35:462-463(2004).
Anim. Genet. 35:462-463(2004).
-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                       22 VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLLSLSKWDQTLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15566470; DOI=10.1111/j.1365-2052.2004.01186.x; Vallinoto M., Schneider M.P., Silva A., Iannuzzi L., Brenig B.; "Molecular cloning and analysis of the swamp and river buffalo leptin
                                                                                                                                                                  1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2006 (Rel. 47, Last annotation update)
Leptin precursor (Obesity factor).
Name=LEP; Synonyms=OB;
Name=LEP; Synonyms=OB;
Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laursasatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bubalus.
                                                                                                                            ö
                                                                                Query Match 85.3%; Score 628; DB 1; Length 167; Best Local Similarity 87.0%; Pred. No. 8.3e-50; Matches 127; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leptin.
By similarity.
8524749CD69CAD99 CRC64;
  25 25 R -> Q (in Ref. 2).
166 166 G -> E (in Ref. 2).
167 AA; 18716 MW; 94C666B3069E50B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 628; DB 1;
Pred. No. 8.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY495587; AAS86311.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                          142 TEVVALSRLQGSLQDMLRQLDLSPGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                                                                                                                                                                   TEVVALSRLOGSLODMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMR; Q5J732; 24-167.
INTERPO; IPR012231; Cytokine 4 hlx.
INTERPO; IPR0100065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 1
117 1
167 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=89462;
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DISULFID
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Q5<u>J</u>732;
      CONFLICT
CONFLICT
SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98066799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3; MEDLINE=98066799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3; Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.; Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.; Donest. Anim. Endocrinol. 14:295-303(1997).

-I. FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintenin constency of the adipose mass.

-I. SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 VPIWRVQDDTKTLIKTIVTRISDISHMQSVSSKQRVTGLDFIPGLHPVLSLSKMDQTLAI
              D'Andrea M., Pilla F., Archibald A.L.;
"Structural and expression analysis of Leptin and Melanocortin-4
"Structural and expression analysis of Leptin and Melanocortin-4
succeptor genes in Casertana Swine breed.";
submitted (NOV-2004) to the EMBL/GenBank/DBB databases.
EMBL; AJ865080; CAI23842.1; -; Genomic_DNA.
SWR; OFTIL9; 24-167.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:007165; P:signal transduction; IEA.
InterPro; IPR000065; Leptin.
PERM: PF02024; Leptin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%; Score 627; DB 2; Length 167; 87.0%; Pred. No. 1e-49; ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Adipose tissue;
Simmons J.M., Dyer C.J., Keisler D.H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      22 167 leptin.
167 AA; 18661 MW; 27550E1E0E63814E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB SHEEP STANDARD; PRT; 146 AA. Q28603; P79212; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEVVALSRIQGSIQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 TEVVALSRLÓGALÓDMLRÓLDLSPGC 167
                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 9-125.
                                                                                                                                                                                                                                                                        PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=LEP; Synonyms=OB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
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OB SHEEP
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                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 YQQILTSLPSRNVIQISNDLENLRDLLHLLASSKSCPLPQARALETLESLGGVLEASLYS 141
                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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                -I- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
-I- SUBCELLULAR LOCATION: Secreted (Probable).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.2%; Score 627; DB 1; Length 167; 87.0%; Pred. No. 1e-49; Live 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leptin.
By similarity.
AV -> GP (in Ref. 8).
I -> L (in Ref. 8).
A -> R (in Ref. 4).
%; 27550EIEOEG3814E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 EMBL; U63540; AAB05923.1; -; mRNA.
EMBL; U59894; AAB05923.1; -; mRNA.
EMBL; U59894; AAB07458.1; -; mRNA.
EMBL; AF026976; AAB97730.1; -; mRNA.
EMBL; AF052691; AAC06303.1; -; mRNA.
EMBL; AF022856; AAC78147.1; -; mRNA.
EMBL; AF477387; AAC78147.1; -; Genomic_DNA.
EMBL; AF477387; AAL84792.1; -; Genomic_DNA.
EMBL; U40812; AAC48641.1; -; mRNA.
HSSP; P41159; 1AX8.
SWR; Q29406; 24-167.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR010355; Leptin; 1.
PANTHER; PTHR11724; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
Genet. 27:275-278(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.0%
Matches 127; Conservative
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ID QSTIL9_PIG PRELIMINARY;
AC QSTIL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
167
167
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97
122
167 AA;
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Name=LEP;
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NCBI_TaxID=9825;
[1]
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CONFLICT CONFLICT CONFLICT SEQUENCE

Query Match

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the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
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                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101; Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T., Casas B., Wray J.B., White J., Cho J., Fahrenkrug S.C., Bennett G.L. Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J., Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.; "Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle.";
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                        84.8%; Score 624; DB 1; Length 146; 87.0%; Pred. No. 1.6e-49; ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BT020625, AAX08642.1; -; mRNA.
                                                                                                                                                                                           L -> H (in Ref. 2).
A -> G (in Ref. 2).
V -> L (in Ref. 2).
; 19D54C53240968CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                      121 TEVVALSRLOGSLODMLWOLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR010065; Leptin.
PANTHER; PTH11724; Leptin; 1.
PFEm; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                 EMBL; U84247; AAB41786.1; -; mRNA.
ERML; U62123; AAB51033.1; -; mRNA.
HSSP: P41159; 1AX8.
SWR; Q28603; 3-146.
                                                                                                                                                                                                                                  146 AA; 16054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 11:626-630(2001).
                                                                                                                                                            ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSEAE4 BOVIN PRELIMINARY;
QSEAE4;
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.0 Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
TISSUE=Pooled;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=LEP;
                                                                                                                                                                       Obesity.
DISULFID
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                            removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
0bese protein (Fragment).
Ctemopharyngodon idella (Grass carp).
Ctemopharyngodon idella (Grass carp).
Actinopterygii, Nepterygii, Teleostei, Ostariophysi, Cypriniformes;
Cyprinidae; Ctenopharyngodon.
NCBI_TaxID=7959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Сарв
                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dai H., Long L.;
"Molecular cloning and sequence analysis of the obese gene from the Ctencharynchopalyngodon idellus.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS51335; AAT45394.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146;
                                                                                                                                                                                                                       Length 167;
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                                                                                                                                                                                                                                                                      9; Mismatches 10; Indels
                                                                                                                                                                       167 AA; 18663 MW; C9AA16B31AF229CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;
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84.1%; Score 619; DB 2;
Best Local Similarity 84.9%; Pred. No. 4.8e-49;
Matches 124; Conservative 13; Mismatches 9;
                                                                                                                                                                                                                       Score 624; DB 2;
Pred. No. 1.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 AA.
SWR; QSEAE4; 24-167.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000065; Leptin.
Ffam; PP02024; Leptin.
FRINTS; PR00495; LEPTIN.
SEQUENCE 167 AA; 18663 MW; C9AA16B31AF22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEVVALSRIQGSLODMLWQLDLSPGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Job time : 146.498 secs
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                                                                                                                                                                                                                       84.8%;
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Q4VW71;
                                                                                                                                                                                                                                                                      Matches 127; Conservative
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BLOSUM62

Scoring table:

Searched:

Perfect score:

Run on:

Sequence:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08398021
; Patent No. 5594101
; GENERAL INFORMATION:
    APPLICANT: Becker, Gerald W.
    APPLICANT: Hale, John E.
    APPLICANT: MacKellar 1, Warren C.
    TITLE OF INVENTION: ANTI-OBESITY PROTEINS
    NUMBER OF SEQUENCES: 5
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Bli Lilly and Company
    STREET: Lilly Corporate Center/Patent Division
    CITY: Indianapolis
    STATE: Indiana
    COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 736; DB 1;
100.0%; Pred. No. 3.4e-74;
iive 0; Mismatches 0;
US-08-488-223A-4
US-09-147-805-4
US-08-438-431A-4
US-08-488-225A-4
US-09-317-081-17
US-09-377-081-17
US-09-686-647A-4
PCT-US96-01471-4
US-10-679-999-18
US-10-679-999-12
US-10-679-999-12
US-10-679-999-12
US-10-679-999-12
US-08-775-066-2
US-08-775-066-2
US-08-775-066-2
US-08-775-066-2
US-08-775-066-2
US-08-775-066-2
US-08-775-066-2
US-08-788-943A-3
US-08-788-943A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CALVELIGEF, SLEVEN P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X100
TELECOMMUNICATION INFORMATION:
TELEFAM: 317-276-0757
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 146 amino acida
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Best Local Similarity 100.
Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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US-08-398-021-3
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                                                                                                                                                     ; Search time 33.1134 Seconds
  (without alignments)
  364.525 Million cell updates/sec
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Sequence 32,
Sequence 1, A
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                                                                                                                                                                                                                                                                                1 VPIQKVQDDTKTLIKTIVTR.....sRLQGSLQDMLWQLDLSPGC 146
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Sequence 5,
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Sequence 3,
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Sequence 1,
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                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: /cgn2 6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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OTHER INFORMATION: /note= "Trp at position 100 is
OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
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OTHER INFORMATION: /note= "Ala at position 101 is
OTHER INFORMATION: replaced with Ser, Asn, Gly, His, Pro, Thr, or Val"
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APPLICANT: Foster, Lisa K
APPLICANT: Furman, Thomas C
APPLICANT: Furman, Thomas C
APPLICANT: Furman, Thomas C
APPLICANT: Furman, Thomas C
APPLICANT: MacKellar, Warren C
TITLE OF INVENTION: Process for Preparing Obesity Protein
TITLE OF INVENTION: Analogs
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSS: ADDRESSEE: Eli Lilly & Company
STREET: Lidianapolis
CONTY: Indianapolis
CONTY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATIONS STRIEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,104
FILING DATE: 24-MAR-1997
CLASSIFICATION NUMBER: US 08/429,362
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/429,362
FILING DATE: 26-ARP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P
REGISTRATION NUMBER: 36467
REFERENCE/DOCKET NUMBER: 10022A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 3:
SEQUINCE CHARACTERISTICS:
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replaced with Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Ser at position 77 is OTHER INFORMATION: replaced with Ala" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replaced with Arg
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NAME/KEY: Modified-site
LOCATION: 103
OTHER INFORMATION: /note=
OTHER INFORMATION: replace
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATURE
                                                  61 YQQILTSMPSRNVIQISNDLENLRDLIHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYS 120
       YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                             Sequence 5, Application US/08788943A
| Patent No. 5831017
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND TITLE OF INVENTION: FORMULATIONS THEREOF
| NUMBER OF SEQUENCES: 35
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center/Patent Division CITY: Indianapolis
| STREET: Indiana
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 736; DB 1; Length 146; 100.0%; Pred. No. 3.4e-74; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USAN
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,943A
FILING DATE: 24-JAN-1997
GIASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P
REGISTRATION NUMBER: X10540
FREFERENCE/DOCKET NUMBER: X10540
TELEPAX: (317) 276-0757
TELEPAX: (317) 277-1917
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                            TEVVALSRIQGSLQDMLWQLDLSPGC 146
                                                                                                                                         121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TEVVALSRIQGSIQDMIWQLDLSPGC 146
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US-08-823-104-3
; Sequence 3, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 146; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                          US-08-788-943A-5
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61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
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Sequence 6, Application US/08648262

Sequence 6, Application US/08648262

Sequence 6, Application US/08648262

Sequence 6, Application US/08648262

Sequence 6, Application

APPLICANT: Bailon, Pascal Mr.

APPLICANT: Campfield, Arthur Dr.

APPLICANT: Guisez, Yves Dr.

TITLE OF INVENTION: Pegylated Obese (OB) Proteins

NUMBER OF SECUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Hoffmann-La Roche, Inc.

STREET: AJO Kingsland Street

CITY: Neutley

STREET: New Jersey

COUNTRY: U.S.A.

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/648,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 736; DB 1; Best Local Similarity 100.0%; Pred. No. 3.4e-74; Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TEVVALSRIQGSLODMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,777
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Picut, Catherine A
REGISTRATION NUMBER: 37419
REFERENCE/DOCKET NUMBER: 9165
TELEPHONE: (201) 235-4387
TELEPHONE: (201) 235-4387
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Epetein, William H.
REGISTRATION NUMBER: 20008
REPRERNCE/POCKET NUMBER: 928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-3323
TELEFAX: (201) 235-333
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ANTI-SENSE: NO
US-09-003-081-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 138
CTHER INFORMATION: /note= "Trp at position 138 is
CTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
US-08-823-104-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                   FEATURE:
NAMES/KEY:
MANGIFIED-Site
LOCATION: 100
OTHER INFORMATION: /note= "Thr at position 106 is
OTHER INFORMATION: /note= "Thr at position 106 is
OTHER INFORMATION: /note= "Leu at position 107 is
OTHER INFORMATION: /note= "Leu at position 107 is
OTHER INFORMATION: replaced with Pro"
FRATURE:
NAMES/KEY: MODIFIED-Site
LOCATION: 111
OTHER INFORMATION: /note= "Gly at position 111 is
OTHER INFORMATION: replaced with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLESSENT ADDRESSES:
ADDRESSES:
ADDRESSES:
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
FILING DATE:
FILING DATE:
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Sequence 6, Application US/09003081

Patent No. 5968779

GENERAL INFORMATION:

APPLICANT: Campfield, Arthur Dr.

APPLICANT: Campfield, Arthur Dr.

APPLICANT: Caujaz, Yves Dr.

TILLE OF INVENTION:

TILLE OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                    LOCATION: 105
OTHER INFORMATION: /note= "Glu at position 105 is
OTHER INFORMATION: replaced with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: Modified-site
LOCATION: 118
COTHER INFORMATION: /note= "Gly at position 118 is
OTHER INFORMATION: repaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 736; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0;
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NAME/KEY: Modified-site
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                                                                                                                                                                                                                           1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                               Gape
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Patent No. 6377893
GENERAL INFORMATION:
APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
                                                                                                                            Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 146;
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                                                                                                                                                                             Indels
                                                                                                                            100.0%; Score 736; DB 2;
100.0%; Pred. No. 3.4e-74;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 736; DB 2; Best Local Similarity 100.0%; Pred. No. 3.4e-74; Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: leptin
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-914-375C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                TEVVALSRLOGSLODMLWQLDLSPGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-Aug-1997
CLIASSIFICATION: 702/20
TELECOMMUNICATION: TROCKMUNICATION: TROCKMUNICATION: 352 392 7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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                                                                             US-08-648-263-6
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                                                                                                                                                                                                                                                                                                                                                                               1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                         1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                  Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08648263
Patent No. 6025325
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Devos, Rene
APPLICANT: Guisez, Yves
TITLE OF INVENTION: RECOMBINANT OBESE (OB) PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFFmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/648,263

FILING DATE: 15-MAY-1996

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,629

FILING DATE: 07-JUN-1995

PILING DATE: 07-JUN-1995

PILING DATE: 07-MAY-1996

APPLICATION NUMBER: US 08/435,777

FILING DATE: 05-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: KEASIST. Lewis J

REGISTRATION NUMBER: 38522

REGISTRATION NUMBER: 38522

REGISTRATION NUMBER: 38524

REGISTRATION NUMBER: 38524
                                                                                                                                                                                                                                                                       ; Score 736; DB 2;
; Pred. No. 3.4e-74;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TEVVALSRLOGSLODMLWQLDLSPGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 Kingsland Street
                                                                                                       not relevant
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 146; Conservative 0
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TOPOLOGY: unknown
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Nutley
STATE: New Jer
COUNTRY: USA
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                                                                                                                                                                                                    ; ANTI-SENSE: NO
US-08-648-262-6
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61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                APPLICANT: HORI, NOBUAKI
APPLICANT: HORI, NOBUAKI
APPLICANT: HORI, NOBUAKI
APPLICANT: SHRAKSHI, TAKEWASA
APPLICANT: TAKEDA, HIROSHI
APPLICANT: TAKEDA, HIROSHI
APPLICANT: TSUJI, MINORU
APPLICANT: TSUJI, MINORU
APPLICANT: MATSUMIYA, TERUHIKO
TITLE OF INVENTION' DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
FILE REFERENCE: YAMA-100
CURRENT APPLICATION NUMBER: US/09/200,919
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 736; DB 2; Length 146; 100.0%; Pred. No. 3.4e-74;
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NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyd disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATINO SYSTEM: PC-DOS/MS-DOS

OFFRANTION DATA:

FILING DATE:

FILING DATE:

FLING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-00952-2
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                                                  121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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                                                                                                                                                                                                    ; Sequence 1, Application US/09200919; Patent No. 6518235; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 146; Conservative
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 146
                                                                                                                                                                                      US-09-200-919-1
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GEGG, COLIN
APPLICANT: GEGG, COLIN
APPLICANT: KINSTLER, OLAF
TITLE OF INVENTION: SITE-DIRECTED DUAL PEGYLATION OF PROTEINS FOR IMPROVED
TITLE OF INVENTION: BIOACTIVITY AND BIOCOMPATIBILITY
FILE REFERENCE: A-567
CURRENT APPLICATION NUMBER: US/09/172,644
NUMBER OF SEQ ID NOS: 1998-10-14
NUMBER OF SEQ ID NOS: 2.0
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Patent No. 6451346
GENERAL INFORMATION:
APPLICANT: SHAH, SUBODH
APPLICANT: BAI, WEIGUO
TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
TITLE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
FILE REFERENCE: A-575
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100.0%; Score 736; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
                                                         121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                  121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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Sequence 1, Application US/09172644
Patent No. 6420339
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US-09-221-178-1
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                                                                                                                                                                                                                                                Length 147;
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APPLICANT: Mackellar, Warren C.
TITLE OF INVENTION: Process For Preparing Anti-Obesity
TITLE OF INVENTION: Process For Preparing Anti-Obesity
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: 11 Lilly and Company/Patent Division
STREET: Lilly Corporate Center
CITY: Indianapolis
STREET: Indiana
STATE: Indiana
COUNTRY: United States
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,362
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 736; DB 1; Best Local Similarity 100.0%; Pred. No. 3.5e-74; Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                             100.0%; Score 736; DB 2; 100.0%; Pred. No. 3.5e-74;
                                                                                                                                                                                                                                                                                             0; Mismatches
; CURRENT APPLICATION NUMBER: US/09/200,919; CURRENT FILING DATE: 1998-11-30; NUMBER OF SEQ ID NOS: 6; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 4; LENGTH: 147; TYPE: PRT ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVVALSRLOGSLODMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 TEVVALSRLQGSLQDMLWQLDLSPGC 147
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ATTORNEY AGRAN INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE, POCKET NUMBER: X.0022
TELECOMMUNICATION INFORMATION:
TELEPRAX: (317) 276-0757
TELEPRAX: (317) 277-1937
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/08429362
; Patent No. 5614379
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Best Local Similarity
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     100.0%; Score 736; DB 4; Length 146; 100.0%; Pred. No. 3.4e-74; ive 0; Mismatches 0; Indels (
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Patent No. 6518235
GENERAL INFORMATION:
APPLICANT: OCMURA, YUTAKA
APPLICANT: SHIRAISHI, TAKEMASA
APPLICANT: SHIRAISHI, TAKEMASA
APPLICANT: TAKEDA, HIROSHI
APPLICANT: TEUSHINA, TERUHIKO
TITLE OF INVENTION: BRUG FOR IMPROVEMENT OF BRAIN FUNCTION
FILE REFERENCE: YAMA-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Anti-Obesity Proteins
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: PCT/US96/00952
                                                                                                                                                                                                                                                                                                                         TEVVALSRLQGSLQDMLWQLDLSPGC 146
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SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
Query Match
Best Local Similarity 100.(
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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PCT-US96-00952-3
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US-09-200-919-4
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123 TEVVALSRLQGSLQDMLWQLDLSPGC 148
                            121 TEVVALSRLOGSLODMLWQLDLSPGC 146
                                                                                                                                     Search completed: May 4, 2006, 21:58:25
Job time : 34.1134 secs
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                                                                          61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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3 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 62
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GENERAL INFORMATION:

APPLICANT: Atkinson, Paul R
APPLICANT: Foster, Lisa K
APPLICANT: Forman, Thomas C
APPLICANT: MacKellar, Warren C
TITLE OF INVENTION: Process for Preparing Obesity Protein
TITLE OF INVENTION: Analogs
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly & Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 736; DB 1; Length 148; Best Local Similarity 100.0%; Pred. No. 3.5e-74; Matches 146; Conservative 0; Mismatches 0; Indels C
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATE: IBM PC COMPATIBLE
COMPATE: IBM PC COMPATIBLE
COURRENT APELICATION DATA:
APPLICATION NUMBER: US/08/823,104
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/429,362
ATTOMING PATE: 26-APR-1995
RIDN DATE: 26-APR-1995
ATTOMING DATE: 26-APR-1995
ATTOMING DATE: 26-APR-1995
ATTOMING DATE: 26-APR-1995
ATTOMING DATE: 26-APR-1995
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; Sequence 18, Application US/08823104
; Patent No. 5840517
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REGISTRATION NUMBER: 36467
REPERENCE/DOCKET NUMBER: 1002
TELECOMMUNICATION INFORMATION:
TELEPAN: 317-277-8110
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FRAGMENT TYPE: N-terminal
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Sequence 4, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appli
Sequence 67, Appli
Sequence 67, Appli
Sequence 14, Appli
Sequence 2482, Appli
Sequence 2482, Appli
Sequence 17, Appli
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Sequence 170, App
Sequence 171, App
Sequence 63, Appl
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Sequence 127, App
Sequence 1, Appli
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Sequence 10, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
                                                                                                     (without alignments)
540.393 Million cell updates/sec
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1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 146
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                                                                                     May 4, 2006, 21:57:29 ; Search time 112.887 Seconds
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-139-794-10

US-10-19-794-10

US-10-622-998-1

US-10-628-98-1

US-10-628-98-1

US-10-628-98-1

US-10-628-98-1

US-10-628-98-1

US-10-628-98-1

US-10-628-189-1

US-10-872-198-127

US-10-872-198-127

US-09-788-189-1

US-09-788-528-7

US-09-788-528-7

US-09-788-788-1

US-10-788-117

US-10-788-1177

US-10-78-180-168

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169

US-10-775-180-169
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                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 10, Application US/10139794
Publication No. US20030232421A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.
APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.
APPLICANT: PIETE Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun L TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)
TITLE OF INVENTION NUMBER: US/10/139,794
CURRENT APPLICATION NUMBER: US/10/139,794
PRIOR PLING DATE: 2002-05-06
PRIOR APPLICATION UMBER: US 60/288,885
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 2930
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108, App
115, App
118, App
115, App
110, App
112, App
112, App
112, App
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Sequence 1
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Sequence 2
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Sequence 9
Sequence 1
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TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL ITILE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL ITILE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE PILE REFERENCE: A-575 CURRENT APPLICATION NUMBER: US/10/191,377

CURRENT FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 146;
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100.0%; Pred. No. 4.3e-72;
ive 0; Mismatches 0;
US-10-756-149-5381
US-10-775-204-551
US-10-775-204-555
US-10-775-204-558
US-11-060-291-1
US-10-893-115-108
US-10-679-999-15
US-10-679-999-15
US-11-054-085-18
US-11-054-085-18
US-11-054-085-18
US-11-054-085-18
US-11-054-085-18
US-11-054-085-12
US-11-054-085-12
US-11-054-085-12
US-11-054-085-12
US-11-054-085-12
US-09-859-361-2
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Publication No. US20030099709A1
GENERAL INFORMATION:
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Matches 146; Conservative
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APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Callies, Stephen D.
TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as FC
TITLE OF INVENTION: Fusion Proteins
FILE REFERENCE: LEX.008
CURRENT APPLICATION NUMBER: US/10/419,058
CURRENT APPLICATION NUMBER: US/09/479,508
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 1050-01-07
PRIOR FILING DATE: 1050-01-07
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                          61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                PEATURE:
OTHER INFORMATION: Translation of SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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Publication No. US20040053366A1
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1 SEQ ID NO 10 LENGTH: 146
                                                                                             ORGANISM: Homo Sapiens
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Sequence 1, Application US/10467114 Publication No. US20040072219A1 GENERAL INFORMATION:

US-10-467-114-1

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Sequence 1, Application US/10622998

Publication No. US20040105840A1

GENERAL INFORMATION:

APPLICANT: Kinstler, Olaf

APPLICANT: Ladd, David

APPLICANT: Papisov, Mikhail

TITLE OF INVENTION: POLYMER

TITLE OF INVENTION: POLYMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
TITLE OF INVENTION: IMMUNOGENICITY
TITLE OF INVENTION: IMMUNOGENICITY
TITLE OF INVENTION: MRC 115
CURRENT APPLICATION NUMBER: BP 01102618.4
PRIOR APPLICATION NUMBER: BP 01103954.2
PRIOR APPLICATION NUMBER: BP 01103954.2
PRIOR PAPLICATION NUMBER: PC1/EP02/01188
PRIOR PRILING DATE: 2001-02-06
PRIOR PRILING DATE: 2001-02-19
PRIOR PELLING DATE: 2002-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 736; DB 4;
100.0%; Pred. No. 4.3e-72;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/10/622,998
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR FILING DATE: 2002-07-19
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SOFTWARE: PatentIn version 3.1
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Matches 146; Conservative
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CRGANISM: Homo sapiens
US-10-622-998-1
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APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMEIBR
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.000204
CURRENT PELING DATE: 2004-06-18
FRIOR PILING DATE: 2004-06-18
PRIOR PILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR PILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: BP 04003058
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
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100.0%; Score 736; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 736; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0;
                   PRIOR FILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 2036
SEQ ID NO 1
SEQ ID NO 1
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APPLICANT: Andre KOLTERMANN
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CORGANISM: Homo sapiens
US-10-872-198-127
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US-10-468-496-1
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 146
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Use, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT PILING DATE: 2003-09-09
FRIOR FILING DATE: 2003-03-21
FRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FRASEQ for Windows Version 4.0
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APPLICANT: Carter Graham
APPLICANT: Carter Graham
APPLICANT: JOSE, Tim
APPLICANT: JOSE, Tim
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: BETHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
FILE REFERENCE: MER-117
CURRENT APPLICATION: NUMBER: US/10/468,496
CURRENT PILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR FILING DATE: 2001-02-19
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100.0%; Score 736; DB 4; Length 14
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels
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DATABASE ENTRY DATE: 1995-01-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DAIABASE ENIKI
US-10-658-834A-211
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LENGTH: 146
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APPLICANT: ACCTEMANN, Andre
APPLICANT: SCHEIDIG, Andreas
APPLICANT: SCHEIDIG, Andreas
APPLICANT: SCHEIDIG, Andreas
APPLICANT: Corostation of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 736; DB 5; 100.0%; Pred. No. 4.3e-72;
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100.0%; Pred. No. 4.3e-72;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Artificial linker US-10-502-344-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 127, Application US/11021951; Publication No. US20050175581A1
GENERAL INFORMATION:
APPLICANT: HAUPTS, Ulrich
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 146; Conservative
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Best Local Similarity 100.
Matches 146; Conservative
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US-11-021-951-127
                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pa
                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10623189
; Sequence 1, Application US/10633189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
    APPLICANT: DEPAOLI, Alex M.
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu.
; TITLE OF INVENTION: DEPOIL OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT;
; PRIOR PELICATION NUMBER: US 10/279,129
; PRIOR PELICATION NUMBER: US 60/336,394
; PRIOR PILING DATE: 2002-10-22
; PRIOR PILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; SEQ ID NO 1
                                                                                                                                                                                              61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                         1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
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   1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSS, Richard
APPLICANT: RATYMIUK, Peter
APPLICANT: SAYERS, Jon
TITLE OF INVENTION: Polypeptide Variants
FILE REPERENCE: 100042.55084US
CURRENT APPLICATION NUMBER: US/10/502,344
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: PCT/GB03/00253
PRIOR FILING DATE: 2003-01-24
PRIOR PPLICATION NUMBER: GB 0201679.8
                                                                                                                                                                                                                                                                                                                                       121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                             TEVVALSRIQGSLQDMLWQLDLSPGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-502-344-22
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61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                        APPLICANT: Spurlock, Michael E.
TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
SEQUENCES CODING THEREFOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: ISM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite 2100 111 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 736; DB 3;
100.0%; Pred. No. 5.1e-72;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/928,522
PILLING DATE: 13-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/688,908
FILLING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,830
REGISTRATION NUMBER: PM-8808
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-928-522-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
                                    142 TEVVALSRLOGSLODMLWQLDLSPGC 167
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121 TEVVALSRLQGSLQDMLWQLDLSPGC
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Patent No. US20020142456A1
GENERAL INFORMATION:
APPLICANT: Hernday, Natasha
                                                                                                                                                    Sequence 7, Application US/09928522; Patent No. US20020110857A1; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 53202
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Wisconsin
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-789-306-3
                                                                                                                                   US-09-928-522-7
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TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YOOILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                        61 YQQILTSMPSRNVIQISNDLENLRDLIHVLAFSKSCHLPWASGLBTLDSLGGVLRASGYS 120
                        YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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COMPUTER: IEBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/736,084
FILING DATE: 13-Dec-2000
CLASSIFICATION SUMBER: 08/438,431
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 1995,
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 1995
APPLICATION NUMBER: 08/292,345
FILING DATE: No. 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 66,742
TELEFAK: 201343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-736-084-4
                                                                                                                    121 TEVVALSRLOGSLODMLWQLDLSPGC 146
                                                                                                                                                         121 TEVVALSRLÖGSLÖDMLWÖLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                Sequence 4, Application US/09736084 Patent No. US20020107211A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
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Best Local Similarity 100.
Matches 146; Conservative
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US-09-736-084-4
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22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILLTLSKMDQTLAV 81
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Patent No. US20020155100A1
GENERAL INFORMATION
APPLICANT: KIEFFER, TIMOTHY J.
APPLICANT: CHEUNG, ANTHONY T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
FILE REFERENCE: 0.29996/027 8721
CURRENT APPLICATION NUMBER: US/09/804,409A
CURRENT APPLICATION NUMBER: US/09/804,409A
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 736; DB 3; Length 167; 100.0%; Pred. No. 5.1e-72; tive 0; Mismatches 0; Indels (
                                                    CORRESPONDED AMORES:
ADDRESSE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
CONTRY: U.S.A.
ZONPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,306
FILING DATE: 20-Feb-2001
CLASSIFICATION: <underween
TITLE OF INVENTION: Canine OB Protein Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

**APPLICATION WINBER: 08/609,408

FILING DATE: «UNKNOWN»

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Eggert, Joan D.
REFERENCE/DOCKET NUMBER: A-387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: -21 to -1 SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-789-306-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leader Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 146; Conservative
                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 11
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match 100.0%; Score 736; DB 3; Length 167; Best Local Similarity 100.0%; Pred. No. 5.1e-72; Matches 146; Conservative 0; Mismatches 0; Indels
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Sequence 19, Appl Sequence 211, Appl Sequence 32, Appl Sequence 47, Appl Sequence 66, Appl Sequence 672, Appl Sequence 671, Appl Sequence 671, Appl Sequence 671, Appl Sequence 671, Appl Sequence 672, Appl Sequence 672, Appl Sequence 672, Appl Sequence 674, Appl Sequence 674, Appl Sequence 675, Appl Sequence 675, Appl Sequence 675, Appl Sequence 679, App
                                                                                                                                                 May 4, 2006, 21:58:39; Search time 18.0619 Seconds (without alignments) 374.135 Million cell updates/sec
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1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 146
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1: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pepl:*
2: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
9: /SIDS5/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/USII_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/USII_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/USII_NEW_PUB.pep:*
12: /SIDS5/ptodata/2/pubpaa/USII_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-176-830-211
US-11-236-1932-213-1332
US-10-192-219-47
US-11-192-219-47
US-11-176-830-666
US-11-176-830-677
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US-11-176-830-673
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US-11-176-830-678
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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ALIGNMENTS

```
APPLICANT: CHUNG, YONG-HOON
APPLICANT: LEE, Hak-sup
APPLICANT: LEE, Hak-sup
APPLICANT: XI, K1-wan
APPLICANT: XI, K1-wan
APPLICANT: XI, K1-wan
APPLICANT: KIM, Jac-Youn-Hwan
APPLICANT: HEO, Youn-Hwan
APPLICANT: HEO, Youn-Hwan
APPLICANT: HEO, Youn-Hwan
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
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US-10-519-390-19
i Sequence 19, Application US/10519390
j Publication No. US20060008872A1
i GENERAL INFORMATION:
APPLICANT: MEDEXGEN Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 146; Conservative
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Sequence 1384, Application US/10821234
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
    APPLICANT: Stache-Crain, Birgit
    APPLICANT: Andarmani, Susan
    APPLICANT: Andarmani
    APPLICANT: Andarmani
    APPLICANT: Andarmani
    APPLICA
                                                                                                                                                                                                                                                                                                                                                                                         61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                   100.0%; Score 736; DB 11; 100.0%; Pred. No. 2.8e-65;
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100.0%; Score 716; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.2e-65;
Matches 146; Conservative 0; Mismatches 0;
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Publication No. US20050272656A1
GENERAL INFORMATION:
TITLE OF INVENTION: USES FOR WSX LIGANDS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS 7
ADDRESSEG Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
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                                                                                                                                                                             Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-236-198-32
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-821-234-1384
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                                                                             **Sequence 211, Application US/11176830
**Publication No. US20060020116A1
**Publication No. US20060020116A1
**GENERAL INFORMATION:
**APPLICANT: Gantier.** Rene
**APPLICANT: Guyon, Thierry
**APPLICANT: Guyon, Thierry
**APPLICANT: Drittanti, Lila
**APPLICANT: Drittanti, Lila
**APPLICANT: Vega, Manuel
**TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
**TITLE OF INVENTION: Acid Molecules and Related Applications
**FILE REFERENCE: 17109-012002 (922B)
**TITLE OF INVENTION NUMBER: US/11/176,830
**CURRENT FILING DATE: 2003-09-08
**PRIOR FILING DATE: 2003-09-08
**PRIOR PILING DATE: 2003-09-08
**PRIOR PRILING DATE: 2003-09-09
**NUMBER OF SEQ ID NOS: 1306
**SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VESULUIS 3

VESULUIS 3

VESULUIS 3

Sequence 32, Application US/11236198

PUBlication No. US20060030530A1

GENERAL INFORMATION:

APPLICANT: Yen, Frances

APPLICANT: Bitain, Bernard

APPLICANT: Fruebis, Joachim

APPLICANT: Bihain, Bernard

TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the

TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the

TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the

TITLE OF INVENTION: MARIBER: US/11/236,198

FILE REFERENCE: 70.US2.REG

CURRENT FILING DATE: 2005-09-27

PRIOR APPLICATION NUMBER: US/09/668,558

PRIOR APPLICATION NUMBER: 60/155,506

PRIOR APPLICATION NUMBER: 60/155,506

PRIOR PILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 32

LENGTH: 167

LENGTH: 167
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100.0%; Score 736; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATABASE ACCESSION NUMBER: Genbank AAA60470 DATABASE ENTRY DATE: 1995-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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PUBLICATION INFORMATION:
                                                                         US-11-176-830-211
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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Used, Manuel
TITLE OF INVENTION: Acid Molecules and Related Applications
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT PILING DATE: 2005-07-06
PRIOR PILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FRAUES (FOR Mindows Version 4.0)
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                                                                                                                                                                                                                                                                                                    61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                  61 YQQILTSMPSRNVIQISNDLENLRDLHYLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels
                                                                                                   Length 146;
                                                                                                                                                0; Indels
                                                                                           Score 734; DB 11;
Pred. No. 3.7e-65;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 672, Application US/11176830 Publication No. US20060020116A1 GENERAL INFORMATION:
                                                                                             vuery match
Best Local Similarity 99.3%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-11-176-830-677
                                                US-11-176-830-666
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TYPE: PRT
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Sequence 666, Application US/11176830

Publication No. US20060020116A1

Sequence 666, Application US/11176830

Publication No. US20060020116A1

SEQUENCE OF UNCONTION:

APPLICANT: Guyon, Thierry

APPLICANT: Output, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (922B)

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-03-21

PRIOR FILING DATE: 2003-03-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/192,219
FILING DATE: 27-Jul-2005
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 736; DB 11; Best Local Similarity 100.0%; Pred. No. 8.8e-65; Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 APPLICATION DAILS
FILING APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Unn-1996
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wenddy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELEFONICATION INFORMATION:
TELEFNONE: 415/225-1994
TELEFNONE: 415/225-1994
TELEFNONE: 415/31-1768
INFORMATION FOR SQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 397 amino acids
TYPE: Amino Acid
                             ZIP: 94080
COMPUTER READABLE FORM:
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Sequence 665, Application US/11176830
; Sequence 665, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
APPLICANT: Gantier, Renee
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Wega, Manuel
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (9228)
CURRENT APPLICATION NUMBER: 10/658,834
FRICK APPLICATION NUMBER: 10/658,834
FRICK APPLICATION NUMBER: 60/457,135
FRICK FILING DATE: 2003-03-21
FRICK FILING DATE: 2003-03-21
FRICK FILING DATE: 2002-09-09
; WUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FRAESEQ for Windows Version 4.0
; TENNERS FRAESEQ for Windows Version 4.0
; TENNERS FRAESEQ FOR WINDOWS: 1306
; SEQ ID NO 665
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Sequence 671, Application US/11176B30
Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gartier, Lila
APPLICANT: Oriteanti, Lila
APPLICANT: Driteanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 1700 VUMBER: US/11/176,830
CURRENT APPLICATION NUMBER: US/658,834
PRIOR PILING DATE: 2003-09-08
PRIOR PRILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-03-21
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                                                                            61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                  YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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Pred. No. 4.7e-65;
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US-11-176-830-665
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Best Local Similarity
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US-11-176-830-665
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| Sequence 683. Application US/20116A1
| Sequence 683. Application No. US20060020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier, Rene
| APPLICANT: Guyon, Thierry
| APPLICANT: Use, Manuel
| TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu | TITLE OF INVENTION: Acid Molecules and Related Applications
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| FILE REFERENCE: 17109-012002 (922B) |
| CURRENT APPLICATION NUMBER: 10/658,834 |
| PRIOR APPLICATION NUMBER: 60/457,135 |
| PRIOR APPLICATION NUMBER: 60/457,135 |
| PRIOR PILING DATE: 2003-03-21 |
| PRIOR FILING DATE: 2003-03-21 |
| PRIOR FILING DATE: 2003-09-09 |
| WUMBER OF EGG ID NOS: 1306 |
| SOFTWARE: FastEEQ for Windows Version 4.0 |
| SEQ ID NOS 683 |
| PRIOR FILING DATE: 2003-09-09 |
| PRIOR PRIOR DATE: 2003-09-09 |
| PRIOR
                          APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Molecules and Related Applications
FILE REPERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT APPLICATION NUMBER: 10/658,834
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR PILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-03-03-17
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.7%; Score 734; DB 11; Length 146; Best Local Similarity 99.3%; Pred. No. 3.7e-65; Matches 145; Conservative 1; Mismatches 0; Indels (
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Drittanti, Lila
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US-11-176-830-677
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 673, Application US/11176830

Sequence 673, Application US/11176830

Sequence 673, Application No. US20060020116A1

Sequence 673, Application No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Guyon, Thierry

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (922B)

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT PILING DATE: 2005-07-06

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastEG for Windows Version 4.0

SEQ ID NO 675
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Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                     Score 733; DB 11;
Pred. No. 4.7e-65;
1; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 671
LENGTH: 146
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Best Local Similarity 99.3%;
Matches 145; Conservative
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ORGANISM: Homo sapiens
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US-11-176-830-671
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Sequence 676, Application Us/11176810
Publication No. US200602016A1
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INFORMATION NORSE: GO(409, 898
FRIOR FELLINO DATE: JOSE-30166
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INFORMATION NORSE: GO(409, 898
FRIOR FILINO DATE: JOSE-30166
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Sequence 36, Application US/11236198

Publication No. US20060030530A1

GENERAL INFORMATION:

APPLICANT: Yen, Frances

APPLICANT: Frickson, Mary Ruth

APPLICANT: Frickson, Mary Ruth

APPLICANT: Fruels, Joachim

APPLICANT: Bihain, Bernard

TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the

TITLE OF INVENTION: MACHODS OF Screening For Compounds That Modulate the

TITLE OF INVENTION: MACHODS OF Screening For Compounds That Modulate the

TITLE OF INVENTION: MACHODS OF SCREENING TITLE OF INVENTION: MACHODS OF SCREENING DATE: 2005-09-27

CURRENT FILING DATE: 2005-09-27

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 106

SECOND TO NOS: 106

SECOND TO NOS: 106

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99.6%; Score 733; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels
Best Local Similarity 99.3%; Pred. No. 4.7e-65; Matches 145; Conservative 1; Mismatches 0; Indels
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Job time : 19.0619 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQ ID NO 36
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-11-236-198-36
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

Run on:

4, 2006, 21:46:23 ; Search time 137.526 Seconds (without alignments) 463.258 Million cell updates/sec

US-10-623-189-2 731 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 145 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* geneseqp2005s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw00302 Human del	Aaw00541 Human mat	Aaw30893 Synthetic	Aay92815 Mature le	Aay83769 Human OB	Aay97889 Mutant ma	_	_	Abr57163 Recombina	Aaw34397 Human Met	Aay97890 Mutant ma	Aay92262 Mature re	Aaw00537 Human obe	_	Aaw00525 Human obe	Aaw00530 Human obe	Aaw00532 Human obe	Aaw00531 Human obe	Aaw00523 Human obe	Aaw00533 Human obe	Aab28450 Human OB	Aay87728 Murine OB	Aab28469 Human OB	Abg74166 Human obe
SUMMARIES	OI.	AAW00302	AAW00541	AAW30893	AAY92815	AAY83769	AAY97889	AAY95787	AAB14266	ABR57163	AAW34397	AAY97890	AAY92262	AAW00537	AAW00515	AAW00525	AAW00530	AAW00532	AAW00531	AAW00523	AAW00533	AAB28450	AAY87728	AAB28469	ABG74166
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Abb84118 Truncated Abu64563 Human obe Ade93139 Human ob Abb84141 Truncated		Aaw00013 Acid Btab Aar99490 Chimeric Aaw00539 Human mat	Aaw30892 Synthetic Aaw34482 Human obe Aaw08595 Properly		Aaw22900 Biologica Aaw22901 Biologica Aaw30791 Obesity p	Aaw26191 Obesity p Aaw26194 Obesity p
ABB84118 ABU64563 ADT93139 ABB84141	ABB84140 ABB84139 AAW34396	AAW00013 AAR99490 AAW00539	AAW30892 AAW34482 AAW08595	AAW22896 AAW08599 AAW10151	AAW22900 AAW22901 AAW30791	AAW26191 AAW26194
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25 27 28	330	ო ო ო თ ო 4	36	38 39 40 40	4 4 4 1 2 6	4 4 5

ALIGNMENTS

RESULT 1

Human; obesity protein; ob; fat cell cDNA library; primer; PCR; polymerase chain reaction; amplify; dipeptide leader; antibody; peripheral adipose tissue; weight gain; obese; peptide hormone; fat deposit; type II diabetes; cardiovascular disease; cancer. AAW00302 standard; protein; 145 AA. Human delta Gln28 ob protein. 95US-00384493. 95US-00451250. 96WO-US001411. (first entry) Schoner BE; (ELIL) LILLY & CO ELI. WO9624670-A1. Basinski MB, 29-JAN-1996; 06-FEB-1995; 26-MAY-1995; Homo sapiens 20-NOV-1996 15-AUG-1996. AAW00302;

WPI; 1996-384442/38. N-PSDB; AAT40259, AAT40260.

New DNA encoding two forms of the human obesity gene product - and related vectors and transformed cells, used to produce recombinant proteins for treating obesity.

Claim 4; Page 23; 30pp; English.

The sequences given in AAW00301-02 represeent two forms of the human obesity protein, ob, in which Ala27Gln28 in AAW00301 are replaced by a single Thr in AAW00302. The nucleic acid sequences were isolated from a human fat cell cDNA library using the primer sequences given in AAT40261-64. The ob proteins are pref. expressed with a dipeptide leader sequence of Met-Arg or Met-Tyr. Experiments have suggested that the ob proteins are released by peripheral adipose tissue and are capable of controlling weight gain in normal and obese mice. The ob proteins are thought to be

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Gaps

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for health or cosmetic reasons in obese humans, or to produce leaner food animals. Antagonists of GBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in humans, or for production of Kobe beef or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in diagnostic immunoassays for the presence of GBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of GBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to monitor treatment of these diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel pharmaceutical composition comprises an obesity protein, e.g. the present sequence, together with sucrose and/or trehalose. The composition can be used to treat obesity and associated disorders, e.g. diabetes,
                                                                                                                                                                                                                                                                                                                                                QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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                                                                                                                                                                                                         100.0%; Score 731; DB 2;
100.0%; Pred. No. 1.8e-72;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW30893 standard; protein; 145 AA
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                                                                                                                                                                                                                                                                                QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
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 circulating peptide hormones which regulate the size of a bodies fat deposits. They can be used to treat obesity and to reduce the risk of type II diabetes, cardiovascular disease and cancer. Anti-ob protein antibodies may be used for diagnostic purposes
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                                                                                                                          Length 145;
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                                                                                                                       ; Score 731; DB 2;
; Pred. No. 1.8e-72;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                 reducing wt. in treatment of diabetes cholesterol and for cosmetic reasons.
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                                                                                       Sequence 145 AA;
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30-NOV-1994;
10-MAY-1995;
07-JUN-1995;
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ile, Val, Ala or Gly"
                                                   1 VPIQKVQDDTKTLIKTLIKTINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                     VPIQKVQDDTKTLLKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
              Gaps
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 Pred. No. 1.8e-72; 
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             Mismatches
                                                                                                                                                                                                                                                                                         Mature leptin receptor agonist analogue.
                                                                                                                                   EVVALSRLQGSLQDMLWQLDLSPGC 145
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 100.0%;
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Local Similarity 100.
nes 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                            AAY92815;
              Matches
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deptin analogues comprise this sequence having at least one substitution as featured above. A glutamine residue may be present at position 28 (see AAVS2712) or absent as in this sequence. A claimed method for preventing the loss of lean tissue mass associated with improper nutrition comprises administering to a mammal a leptin receptor ligand. The leptin receptor ligand is preferably a human leptin receptor agonist, such as the present sequence. Binding of the leptin receptor inhibitor leads to an increase of leptin production and a consequent increase in body mass. The method can be used for therapy in catabolic states such as cachesta resulting from illnesses such as anorexia and malnutrition. Methods of increasing lean tissue growth are also useful in the fields of veterinary science and animal husbandry in benefiting the health and quality of livestock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for preventing the loss of lean tissue mass useful in therapy during catabolic states such as cachexia resulting from illnesses such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 60
                                                                                                                                                                                                                                                                                                                                          /note= "can be replaced with methionine sulfoxide, Leu,
Ile, Val, Ala or Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VPIQKVQDDTKTLIKTINTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
"can be replaced with Ser, Asn, Gly, His, Pro,
                                                                                                                                                                                                                                                                                                                                                                                                  Met,
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                                                                                                                                                                                                                                                                                                                                                                                               note= "can be replaced with Ala, Glu, le, Phe, Tyr, Ser, Thr, Gly, Gln, Val
                                                                                                                                     with Lys or
                                                                                                                                                                                                                                                             note= "can be replaced with Leu"
                                                                                                                                                                                                                                                                                                                       note= "can be replaced with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "can be replaced with Glu"
                                                                         note= "can be replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 731; DB 3;
Pred. No. 1.8e-72;
                                            be replaced with Arg"
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100.0%; Pred. No. 1...
0; Mismatches
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                                               'note= "can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anorexia and malnutrition.
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Best Local Similarity 100.
Matches 145; Conservative
   /note= ".
or Val"
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                                                              Misc-difference 102
                                                                                                                       Misc-difference
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                                 Misc-difference
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The invention relates to a novel dextran-leptin conjugate comprising at least one low molecular dextran moiety, of 1-20 kDa, attached to at least one leptin moiety. The leptin moiety is preferrably the mature human OB protein (AAY83768). That leptin moiety is preferrably the mature human OB protein. Alternatively the leptin may be a homeologue of the human OB protein. Alternatively the leptin may be a homeologue of the human OB protein. This sequence corresponds to the catran-leptin conjugates can be used for weight modulation, treatment or prevention of diabetes, especially Type II, blood lipid reduction, e.g. hyperlipidemia, increasing lean body mass and increasing insulin conjugates may also be used in combination therapies, e.g. prior to heart surgery or liposuction. The dextran-leptin conjugates ensitivity. The conjugates may also be used in combination therapies, e.g. prior to heart surgery or liposuction. The dextran-leptin conjugates have improved efficacy, longer plasma circulation time, and no kidney vacuole formation. Hey also have improved solubility and minimal injection site reactions. (Note: this sequence is not given in the specification but is generated from information given by the inventors)
                         QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLFWASGLETLDSLGGVLEASGYST 120
QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New dextran-like conjugate compositions having improved efficacy and circulation time, increased solubility, and reduction in injection site reactions compared to native human leptin.
                                                                                                                                                                                                                                                                                                                                                                                      Antidiabetic, anorectic, antilipemic, dextran-leptin conjugate, human, mature OB protein; weight modulation; diabetes; blood lipid reduction; hyperlipidemia, lean body mass; insulin sensitivity; heart surgery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 731; DB 3;
ilarity 100.0%; Pred. No. 1.8e-72;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  Human OB mutein (Val22-Cys167-delta(Gln49)).
                                                                                                         EVVALSRLQGSLQDMLWQLDLSPGC
                                                                                                                                                                                                                            AAY83769 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0096194P.
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                                                                                                                                                                                                                                                                                                            21-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-224187/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      liposuction, mutein
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Best Local Similarity
Matches 145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                  AAY83769;
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The invention relates to a dual-PEGylated leptin bioconjugate comprising two polyethylene glycol (PEG) moieties attached site-specifically at two coations in a leptin protein. The invention also provides a site-directed poly-PEGylation strategy for proteins which results in directed poly-PEGylation strategy for proteins which results in chomogenous preparations, and can be used with other biologically active agents including a variety of growth factors and peptide hormones. In leptin, a serine to cysteine substitution was engineered into the protein cat position 77 (relative to the wild-type mature sequence, AAY97871), and the S77 leptin analogue was PEGylated at the engineered cys residue and at the N-terminus. Leptin is a protein which has been shown to cause at the N-terminus. Leptin is a protein which has been shown to cause weight loss in animals, indicating that it will be useful for causing weight loss in humans. However, these studies also indicate that leptin confluence to be administered chronically and in a high concentration in would need to be administered chronically and in a high concentration for midividual, forms precipitates at the injection site, which into midividual, forms precipitates at the injection site, which criggers an inflammatory response. The leptin bioconjugate of the injection site, as seen with prior at leptin compositions. The dual-PEGylated leptin conjugates are used to effect weight cleptin. The dual-PEGylated leptin conjugates are used to effect weight leptin. The dual-PEGylated leptin conjugates are used to effect weight coless, and may also be used to treat type II diabetes and hyperlipidaemia.
                                                                                    New dualPEGylated-leptin bioconjugate useful for treating obesity and diabetes has polyethylene glycol conjugated to two specific sites on the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Leptin analogue; human; polyethylene glycol; site-specific PEGylation; obesity; anorectic; type II diabetes; antidiabetic; hyperlipidaemia; antilipaemic; mutant; mutein.
EVVALSRLOGSLODMLWQLDLSPGC 145
                                                                                                                                                                                  EVVALSRIQGSIQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                       Mutant mature human leptin, delta-Q28.
                                                                                                                                                                                                                                                                                  AAY97889 standard; protein; 145 AA
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leptin molecule.
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Length 145; 0; Indels 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 60

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100.0%;
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Matches 145; Conservative
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Best Local Similarity
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                                                                                                                                                                                                        Sequence 145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1999;
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Leptin 1-145. This is a natural variant of human leptin 1-146 (see
AXY95786) in which residue Gln-28 is absent. The invention is directed to
glycosylated leptin proteins that have a Stokes' radius greater than that
of naturally occurring human leptin. Preferred glycosylated leptins have
look naturally occurring human leptin. Preferred glycosylated leptins have
glycosylation sites at amino acid positions 4, 8, 23, 43, 46, 47, 68, 69,
look of the present sequence to provide
glycosylation sites at amino acid positions 4, 8, 23, 43, 46, 47, 48, 47, 48, 48, 100, 101, 102, 117 and 140, especially 46, 68, 47, 48, 48, 50, 100, 101, 102, 117 and 99, 101, or 2 + 46 + 68, 117, 68 +
coll + 117 and 66 + 102, 68 + 101, 47 + 68 + 1101, 68 + 101, 47 + 68 + 1101, 23, 46 + 68 + 101, 47 + 68 + 1101, 23, 46 + 68 + 101, 47 + 68 + 1101, 23, 46 + 68 + 91, 23 + 46 + 68 + 91, 24 + 66 + 101 and 46 + 68 + 91, 24 + 66 + 101, and 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21 + 46 + 68 + 91, 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    QOILTSMPSRNVIQISNDLENLRDLIHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
Sequences AAY97889-Y97893 represent specifically claimed human mature leptin analoques which may be dually-pesyJated according to the invention. Note: The present sequence is not shown in the specification, but is derived from the mature human leptin sequence given on page 12
                                                                                                                                                                                                                                                                                                                                                                  1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                                                                                                                                                                                                                                                   1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptin, rHu-Leptin 1-145; human; glycosylation; obesity; diabetes; hyperlipidemia; antiobesity; antidiabetic; hyperlipemic; therapy.
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                                                                                                                                                                                                           Length 145;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                           100.0%; Score 731; DB 3;
100.0%; Pred. No. 1.8e-72;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mature recombinant human leptin rHu-Leptin 1-145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVVALSRLQGSLQDMLWQLDLSPGC 145
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                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin FH, Elliott SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-524540/47.
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                                                                                                                                                      Sequence 145 AA;
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as well as vectors and prokaryotic (especially bacterial) or eukaryotic (especially human, monkey, BHK and CHO) host cells useful for recombinant production of the glycosylated leptins. The glycosylated leptins or nucleic acids encoding them, are used in the treatment of obsalty, diabetes and the effects of high blood lipid content (claimed). They have longer systemic circulation times in vivo than native leptins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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thermosensitive hydrogel; protein delivery.
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Pred. No. 1.8e-72;
                                                                                                                                                                                                                                                                                                          100.0%; Score 731; DB 3;
100.0%; Pred. No. 1.8e-72;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EVVALSRLQGSLQDMLWQLDLSPGC 145
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Length 145; Indels 9

Matches

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QQILTSMPSRNVIQISNDLENLRDLLHVLAPSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obesity protein; OB; Met-OB; mouse; human; lean tissue mass; liposuction; athletic performance improvement; implant surgery; insulin sensitivity; cardiac surgery; bone resorption; diabetes; osteoporosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                    QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
been extinguished and the baseline serum concentration of leptin is less than 4 ng/ml. The present sequence represents a recombinant human leptin (rHu-Leptin 1-145), which has a glutamine absent at position 28 of rHu-Leptin 1-146 (see ABRS7162)
                                                                                                                                                                                                                                                                                                                  1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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                                                                                                                                                                                    100.0%; Score 731; DB 6; 100.0%; Pred. No. 1.8e-72; ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 145; Conservative
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                                                                                                                                        Sequence 145 AA;
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                                                                                                                                                          of metabolic
form of lipoatrophy
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                                                            VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                  1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; leptin; recombinant; lipoatrophy; antilipaemic; antidiabetic; antiarteriosclerotic; vasotropic; gene therapy; HIV; HAART; highly active antiretroviral therapy; lipoatrophic; hyperglycaemia; hormone replacement therapy; metabolic abnormality; dyslipidaemia; hyperlipidaemia; hypertlolesterolaemia; hypertlolesterolaemia; hypertlolesterolaemia; atherosclerosis; vascular restenosis; insulin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant human leptin (rHu-Leptin 1-145) protein SEQ ID NO:2.
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of leptin, its analog or derivative for treatment abnormalities associated with lipoatrophy or acquired
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               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2002; 2002WO-US033875
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               145; Conservative
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Homo

water soluble polymer) improves stability, increases circulation time

and/or reduces immunogenicity

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note= "optionally substituted"
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                                                                                                                                                                                                                                                                                                                                                             107
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                                     Misc-difference 77
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Increasing lean tissue content by using obesity protein analogue cosmetic use, to improve athletic performance, increase insulin sensitivity, overall body strength and decrease bone resorption. Claim 1; Page; 50pp; English.

- for

AAW34394-W34401 represent mutations and truncations of the mouse and human obseity (OB) proteins shown in AAW22434 and AAW22435. The OB proteins, and these mutations can all be used in the method of the invention. The method of the invention is for increasing lean tissue mass by administration of an OB analogue. The OB proteins are used for cosmetic applications, to improve athletic performance or as adjunct to surgery (e.g. liposuction or implant surgery, cardiac surgery, treatment of broken bones etc.). OB proteins also increase insulin sensitivity and overall body strength, and decrease bone resorption, e.g. for treating coverall body strength, and decrease bone resorption, e.g. for treating coverall body strength, and decrease bone resorption, e.g. for treating coverall body strength, and decrease bone resorption, e.g. for treating coverall body strength, and decrease bone resorption, e.g. for treating coverall as increased, increased by osteoporosis. Also red blood cell production is increased, increasing mental as well as physical profused in the side effects associated with use of anabolic steroids, growth hormone the side effects associated with use of anabolic steroids, growth hormone etc. Chemical modification of the OB protein (e.g. by attachment to a

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The invention relates to a dual-PEGylated leptin bioconjugate comprising two polyethylene glycol (PEG) moieties attached site-specifically at two conversions in a leptin protein. The invention also provides a site-directed poly-PEGylation strategy for proteins which results in directed poly-PEGylation strategy for proteins which results in compensus preparations, and can be used with other biologically active cagents including a variety of growth factors and peptide hormones. In leptin, a serine to cysteine substitution was engineered into the protein cat position 77 (relative to the wild-type mature sequence, AAY97871), and the N-terminus. Leptin is a protein which has been shown to cause the N-terminus. Leptin is a protein which has been shown to cause weight loss in humans. However, these studies also indicate that leptin would need to be administered chronically and in a high concentration formulation to effectively treat obesity in humans. Leptin is insoluble
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                                                                                                                                                                                                                  QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                        62 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leptin analogue; human; polyethylene glycol; site-specific PEGylation; obesity; anorectic; type II diabetes; antidiabetic; hyperlipidaemia;
                                                                                                                                              1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                                                                                     2 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                                 Gape
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                                                                             Length 146;
                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant mature human leptin, methionyl leptin delta-Q28.
                                                                               100.0%; Score 731; DB 2;
100.0%; Pred. No. 1.8e-72;
                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                          EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                              AAY97890 standard; protein; 146 AA.
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                                                                                                                   Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gegg C, Kinstler O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-329085/28.
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leptin molecule.
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at physiologic pH at relatively high concentrations, and when injected into an individual, forms precipitates at the injection site, which triggers an inflammatory response. The leptin bioconjugate of the invention provides leptin in a form which allows high dosage without the invention provides leptin in a form which allows high dosage without the provides of leptin precipitates and associated inflammatory response at the injection site, as seen with prior art leptin compositions. The dual-psylated leptin molecule is large enough to avoid glomerular filtration and hence kidney vacuolation as seen with a single 20 kDa PEG conjugated leptin. The dual-PEGylated leptin conjugates are used to effect weight loss, and may also be used to treat type II diabetes and hyperlipidaemia. Sequences ANY97899-Y97893 represent specifically claimed human mature leptin analogues which may be dually-PEGylated according to the invention. Note: The present sequence is not shown in the specification, but is derived from the mature human leptin sequence given on page 12
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                                                                                                                                                                                                                                                                                                                   Length 146;
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                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                               100.0%; Score 731; DB 3;
100.0%; Pred. No. 1.8e-72;
iive 0; Mismatches 0;
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/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predisposition; screening; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY92262 standard; protein; 146 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page; 40pp; English
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98US-00181836
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-339110/29.
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Best Local Similarity
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                                                                                                                                                                                                                                                                             Sequence 146 AA;
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27-OCT-1998;
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This is the macure, recombinant method, number leptin 1-145, which is a variant of the Library number method for determining the predisposation of an obesit on 28. The claimed method for determining the predisposation of an obese individual to respond to leptin, leptin analog or derivative treatment comprises determining if the leptin analog or derivative treatment, and ascertaining if the leptin level is in the bottom 25 or 33 percent of leptin levels of coses individuals. The thu-Leptin 1-146 or 1-15 (see AAY92262) or other analogues (e.g. AAY92263-66) may be used in treatment. The method can be used as a screening tool to determine the likelihood that an obese individual (i.e. an individual with a body mass index of greater than 27) not having co-morbidities of obesity, such as administration with weight loss. Leptin is used for weight modulation (especially weight reduction), treatment of diabetes, blood lipid as well as the treatment of conditions associated with fertility, wound healing, hematopoletic conditions, angiogenic conditions and chronic etress conditions. Prescreening an individual prediction, more associated with fertility means the treatment of conditions and individuals predisposition to respond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 121
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                                                                                                                                                                                                                                                                                                                                                                                   to leptin administration may save on unnecessary treatments. Note: The specification provides the sequence of the mature protein which appears on pages 12-13, a methionyl residue is added at position -1 to create this rHu-Leptin 1-145 as described in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VPIQKVQDDTKTLIKTIVTRINDISHISVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 731; DB 3; 1
100.0%; Pred. No. 1.8e-72;
ive 0; Mismatches 0;
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/note= "obesity protein"
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/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 EVVALSRLQGSLQDMLWQLDLSPGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Y18G mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Q20P mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW00537 standard; protein; 165 AA.
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AAM90514 and AAW90515 represent variants of the murine and human obesity polypeptides (OBP), respectively. These sequences lack the Gln residue colypeptides (OBP), respectively. These sequences lack the Gln residue content at position 49 of the wild type sequences (represented by AAR92719 and AAR92720 respectively). OBP (also known as leptin) is a charmone involved in the regulation of body weight. This sequence has creaseful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood presence or high cholesterol. The DNA encoding this sequence (and sequences complimentary coil) can be used in agent therapy for modifying body weight. This opese humans, or to produce leaner food animals. Antagonists of OBP colinoing antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer. Or for cosmetic reasons in thumans, or for production of Kobe beef or Fole gras in domestic animals. Complexed (Ab) can also be used in diagnostic immunosassys for the presence of OBP. The formation of Ab-OBP complexes enables in vitro certaing weight elevals of OBP in a sample, especially to detect diseases evaluation of levals of OBP in a sample, especially to detect diseases
Obesity, mouse; OBP; leptin; hormone; body weight regulation; diabates; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Pole gras; immunoassay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gajiwala K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.
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100.0%; Pred. No. 2.1e-72;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                        /note= "obesity protein"
                                                                                                                                                                                       "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 174; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00292345.
94US-00347563.
95US-00438431.
95US-00483211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROCKEFELLER.
                                                                                                                                                                                                                    .166
                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-099009/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV
                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Friedman JM,
                                                                                                                                                                                                                                                                                   GB2292382-A.
                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1994;
30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                  21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burley SK;
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                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human obesity polypeptides (OBP). This sequence has residues 18-21 mutated in comparison to the wild type sequence has residues 18-21 and AAR9720). OBP (also known as leptin) is a hormone involved in the regulation of body weight. This sequence has effects on both food intake and energy expenditure. OBP and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating clabetees, high blood pressure or high cholesterol. The DNA encoding this sequence (and sequences complimentary to it) can be used in gene therapy for modifying body weight. This protein can be used for reducing weight of modifying body weight. This protein can be used for reducing weight of animals. Antagonists of OBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in humans, or for production of Kobe beef cancer, or for cosmetic animals. OBP antibodies (Ab) can also be used in diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect disasses associated with elevated or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR92725-R92730, and AAW00516-W00537 represent variants of the murine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                            Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 731; DB 2; Length 16
Best Local Similarity 100.0%; Pred. No. 2.1e-72;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       levels, and to monitor treatment of these diseases
                                                                                                                                                                                                                                                                                                            Maffei M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                            Proenca R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW00515 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page ?; 304pp; English.
                                                                                                                                           94US-00292345.
94US-00347563.
95US-00438431.
95US-00483211.
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                                                                                                 95GB-00016947.
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                                                                                                                                                                                                                                                                                                            Friedman JM,
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                                                                                                 17-AUG-1995;
                                                                                                                                                17-AUG-1994;
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10-MAY-1995;
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       GB2292382-A.
                                                     21-FEB-1996
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10-MAY-1995;
07-JUN-1995;
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                                                                                                 Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "obesity protein"
                                                                                                                                                            'note= "signal peptide"
142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                  'note= "L10H mutation"
                                                                                                                                                                                                                                                                                                                  note= "W11S mutation"
                                                                                                                                                                                                                                                                                                                                  note= "L12S mutation"
                                                                                                                                                                                                                                                                                                                                                'note= "W13G mutation"
                                                                                                                                                                                                                                                                                                                                                               'note= "P14L mutation"
                                                                                                                                                                                                                                                                                                                                                                              note= "Y15V mutation"
                                                                                                                                                                                                                                                                                                                                                                                              'note= "L16P mutation"
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "F17R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Y18G mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "V19S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Q20H mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "A21M mutation"
                                                                                                                                                                            note= "H2G mutation"
                                                                                                                                                                                                          note= "G4S mutation"
                                                                                                                                                                                                                                                      'note= "C7H mutation"
                                                                                                                                                                                                                                                                      note= "G8H mutation"
                                                                                                                                                                                                                                                                                     'note= "F9H mutation"
                                                                                                                                                                                           'note= "W3S mutation"
                                                                                                                                                                                                                         note= "T5H mutation"
                                                                                                                                                                                                                                        note= "L6H mutation"
                                                                                                                                             Location/Qualifiers
1. .21
                                      AAW00525 standard; protein; 166 AA.
                                                                                   Human obesity protein variant #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95GB-00016947
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94US-00347563
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                                                                    13-SEP-1996
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                                                                                                                                Synthetic.
                                                     AAW00525
                                                                                                                                                       Peptide
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human obesity polypeptides (OBP). This sequence has the signal peptide thuman obesity polypeptides (OBP). This sequence has the signal peptide thuman obesity polypeptides (OBP). This sequence has the signal peptide (residues 1-21) mutated in comparison to the wild type sequences (represented by AAR92719 and AAR92720). OBP (also known as leptin) is a confidence involved in the regulation of body weight. This sequence has effects on both food intake and energy expenditure. OBP and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood pressure or high cholesterol. The DNA encoding this sequence (and sequences complimentary conics on used in gene therapy for modifying body weight. This opese humans, or to produce leaner food animals. Antagonists of OBP occupations are increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in thumans, or for production of Kobe beef or Foie gras in domestic animals. The presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to monitor treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                       Gajiwala K;
                                                                                                                                                                                                                                                                                                        Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.
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                                                                                                                                                          Halaas JL,
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                                                                                                                                                          Maffei M,
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                                                                                                                                                          Proenca R,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page ?; 304pp; English.
95US-00438431.
95US-00483211.
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                                                                                             ROCKEFELLER
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Best Local Similarity
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Job time : 139.526 secs
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                                                                                          (UYRQ ) UNIV
                                                                                                                                                          Friedman JM,
                                                                                                                                                                                              Burley SK;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 4, 2006, 21:50:51; Search time 27.4055 Seconds Run on:

(without alignments) 509.074 Million cell updates/sec

Title: Perfect score:

US-10-623-189-2 731 1 VPIQKVQDDTKTLIKTIVTR......SRLQGSLQDMLWQLDLSPGC 145 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		leptin precursor -		leptin precursor -	rat ob - rat	glutamate dehydrog	phenylalanine-tRNA	probable myosin he	hypothetical prote	sensory transducti	probable membrane	conserved hypothet	phosphotransferase	internalin, peptid	hypothetical prote	hypothetical prote	carbamoyl-phosphat	probable trehalose	probable soluble l	maltose ABC transp	beta transducin-li	probable membrane	hypothetical prote	prolactin, 20K - M	5,10-methylenetetr	ATP-dependent RNA	hypothetical prote		hypothetical prote
COTURNING	ΩI	153166	LTHU	LTMS	LTRT	155622	AB3281	H71509	T01362	H84583	875514	S46092	G82638	B42374	AB1126	S54039	S46754	A83967	E86305	AI0055	H72282	S76414	S59792	T26551	A28106	D70424	D88511	AD2247	A44267	S44912
	DB	2	Т	٦	٦	~	~	~	~	7	0	~	7		7	~	7	~	~	7	N	N	N	7	~	7	~	~	-	7
	Query Match Length DB	166	167	167	167	167	1600	790	829	952	420	674	186	574	821	444	1228	362	822	639	823	1191	1438	403	177	296	296	348	521	969
ф	Query Match	100.0	98.6	82.6	9.08	90.6	11.4	11.3	11.1	10.8	10.7	10.7	10.6	10.6	10.6	10.5	10.5	10.5	10.5	10.3	10.3	10.3	10.3	10.1	10.1	10.1	10.1	10.1	10.1	10.1
	Score	731	720.5	603.5	589.5	589.5	83	82.5	81.5	79	78	78	77.5	77.5	77.5	77	77	76.5	76.5	75.5	75	75	75	74	73.5	73.5	73.5	73.5	73.5	73.5
	Result No.	-	8	ო	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

leptin precursor - human N;Alternate names: obese protein; obesity factor

RESULT 2

keratin 20, type I 14-nm filament pro	hypothetical proce UDP-N-accetylmuramo hypothetical prote PhoGab protein hom	amino acid ABC tra alkaline phosphata probable exemueles	hypothetical prote geranyltranstransf hypothetical prote	hypothetical prote copper-transportin ribosomal protein esterase XF1743 [1
S37780 JC5625	T47924 AIO517 B84900	D69760 C69676	130031 B70081 B81796 T24722	T40967 S36149 S77486 E82643
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73	72.5	727	72 71.5 71.5	71.5 71.5 71
30 31	8 8 8 6 8 4 8 10	3 B B C	2 6 4 4 2 6 0 11	4 4 4 4 2 6 4 6

ALIGNMENTS

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Tissue in precursor - human
Nighternate names: obese
Ispin precursor - human
Nighternate names: obese
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Date: 01-Nov-1996 #sequence_revision 153166; Gol328
R;Masuzaki, H: Ogawa, Y: Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; In
Diabetes 44, 855-858, 1995
A;Title: Human obses gene expression. Adipocyte-specific expression and regional differ
A;Reference number: I53166; MUID:95309556; PMID:7789654
A;Resion: I53166
A;Resion: Drelliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-166 <RES>
A;Cross-references: UNIPROT:P41159; UNIPARC:UPIO00014D164; GB:D49487; NID:g904211; PIDP
A;Reference number: H01063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-166 <CHE>
A;Residues: 1-166 <CHE>
A;Cross-references: UNIPARC:UPI000014D164; EMBL:U43415; NID:g1163105; PIDN:AAC31660.1;
C;Genetics GB:LEP; OB; OBS
A;Cross-references: GDB:13420; OMIM:164160
A;Cross-references: GDB:13420; OMIM:164160
A;Introns: 48/3
C;Superfamily: leptin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.2e-59;
Matches 145; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVVALSRIQGSIQDMLWQLDLSPGC 145
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lipptin precursor - rat

NiAlternate names: obese protein; obesity factor

C; Saccession: Detail 1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C; Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C; Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C; Accession: Pc4034; Jc4142

R; Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz

Biocham. Biophys. Res. Commun. 211, 469-475, 1995

A; Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial.

A; Reference number: Pc4034

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule and type: mana

A; Molecule type: mRNA

A; Mullance type: mRNA

A; Molecule type: mRN
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 155622
C;Accession: 155622
R;Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; Ti
J. Clin. Invest. 96, 1647-1652, 1995
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                                                                                                                                                                                     60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                                            82 YQQVLTSLPSQNVLQIANDLENLRDLIHLLAFSKSCSLPQTSGLQKPESLDGVLBASLYS 141
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                                                                22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVTGLDFIPGLHPILSLSKMDQTLAV 81
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F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                    142 TEVVALSRLOGSLODILOQUDLSPEC 167
                                                                                                                                                                                                                                                                                                                                                             TEVVALSRLQGSLQDMLWQLDLSPGC 145
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A18952; JE0148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075433; PMID:7984236
A;Accession: A18952
A;Status preliminary; nucleic acid sequence not shown
A;Accession: A18953
A;Status preliminary; nucleic acid sequence not shown
A;Accession: A18953
A;Cross-references: UNIPROT: 44159; UNIPARC:UP10000030BD4; GB:U18915; NID:9623331; PIDN:
R;Liao, H.J; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J: 13, 249-253, 1997
A;Title: Cloning of Ginese obesity gene and construction of prokaryotic expression vect
A;Reference number: JE0148
A;Accession: JE0140
A;Acc
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NyAlternate names: obese protein
C; Species: Mus musculus (house mouse)
C; Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C; Accession: S50863
R; Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A; Title: Positional cloning of the mouse obese gene and its human homologue.
A; Reference number: S50863; MUD:95075453; PMID:7984236
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-167 CZHA
A; Residues: U-167 CZHA
A; Residues: U-167 CZHA
A; Residues: U-168: UNIPROT: P41160; UNIPARC: UPI0000003FAA; EMBL: U18812; NID:9746416; PIE
C; Superfamily: leptin
C; Superfamily: leptin
C; Superfamily: adjone tissue
F; 1-21/Domain: signal sequence #status predicted <NAT>
F; 22-167/Product: leptin #status predicted <NAT>
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A;Gene: At2g34730; T29F13.6
A;Map position: 2
A;Introns: 728/2; 770/3
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A;Title: Molecular cloning of rat obese cDNA and augmented gene expression in geneticall A;Reference number: I55622; MUID:95386724; PMID:7657834
A;Accession: I55622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-167 - REES>
A;Cross-references: UNIPARC:UPI0000038DAF; GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID C;Superfamily: leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AB3281
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: #71509
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: AB3281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1600 «KUR»
A;Cross-references: UNIPROT:Q8YJSS; UNIPARC:UPI0000057BD4; GB:AE008917; PIDN:AAL51413.1;
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamate dehydrogenase (BC 1.4.1.2) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis (c;Date: 01-Feb-2002 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 YQQILTSLPSQNVLQIAHDLENLRDLLHLAFSKSCSLPQTRGLQKPESLDGVLEASLYS 141
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                                                                                                                                                                                                                                         Length 167;
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Similarity 82.9%; Pred. No. 1.7e-46;
21; Conservative 13; Mismatches 11;
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C;Keywords: oxidoreductase
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11.4%; Score 83; DB:
Best Local Similarity 25.6%; Pred. No. 38;
Matches 33; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 TEVVALSRLOGSLODMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 TEVVALSRLQGSLQDILQQLDLSPEC 167
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Best Local Simi
Matches 121; (
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: H71509
A;Accession: H71509
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <ARN>
A;Cross-references: UNIPROT:084481; UNIPARC:UPI0000136445; GB:AE001321; GB:AE001273; NIA;Cross-references: Genome Benefit Companiental source: Serotype D, Strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable myosin heavy chain At2g34730 - Arabidopais thaliana
probable myosin heavy chain At2g34730 - Arabidopais thaliana
probable myosin heavy chain At2g34730 - Arabidopais thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01362; C48760
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaw
Bubmitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A;Reference number: 214179
A;Reference number: 214179
A;Reference number: 214179
A;Reference number: CalubbaJ
A;Reference number: CalubbaJ
A;Residues: 1-829 cROUS
A;Residues: 1-829 cROUS
A;Residues: 1-829 cROUS
A;Residues: DNA
A;Residues: DNA
A;Residues: Caltivar Columbia
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fullio, J. R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A4206
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-829 <STO>
A; Cross-references: UNIPARC:UPI000004A13E; GB: AE002093; NID: 93132472; PIDN: AAC16261.1; C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 TAVEEQAVRVEVPSYRHDIQEETDL--VEBICRTTPFVQKTQKILPTYTPIXSLKRELTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LELSKIRETLLLYHV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY-- 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                         A;Gene: pheT
C;Superfamily: phenylalanine-tRNA ligase beta chain
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 FLANGGLQQFFTYSLLDTEVSSLSLQESSLIPVQNSSWKLRDSLLPG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SLGGVLEASGYS---TEVVALSRLQGSL---QDMLWQL--DLSPG 144
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Best Local Similarity 21.0%; Pred. No. 23;
Matches 33; Conservative 27; Mismatches
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11.3%; Score 82.5; D
Best Local Similarity 27.5%; Pred. No. 17;
Matches 46; Conservative 26; Mismatches
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A;Residues: 1-674 <DUB>
A;Residues: 1-674 <DUB>
A;Residues: 1-674 <DUB>
A;Cross-references: UNIPROT:P38315; UNIPARC:UPI000052EC4; EMBL:236085; NID:9536603; PI
A;Experimental source: strain 5288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein XF1782 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa (5.5pecies: Xylella fastidiosa (5.5pecies: Xylella fastidiosa (5.5pecies: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 (5.5peciession: G82638 R; Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000 A; A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Note: for a complete list of authors see reference number A59328 below
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N.Alternate names: hypothetical protein YBR1505
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: 846092
R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, elumitted to the Protein Sequence Database, August 1994
A;Reference number: 845782
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                                           29 PRLHILL----IEDNLAEARLLQEILKGSPKENF--AFNHVQRLGDALTVLAQGEKFDII 82
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                                                                                                                              94 --SCHLPWASGLETLDSLGG-----VLEASGYSTEVVALSRLQGSLQDMLWQLDLS 142
                                                                                                                                                                   83 LLDLTLPDSQGLNSLPKLQSHPQNLPI1VLTHYQDEELALEAVRQGAQDYLVKRDVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;504-520/Domain: transmembrane #status predicted F;609-626/Domain: transmembrane #status predicted
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A, Cross-references: SGD: S0000420
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                                                                                                                                                                                                                                                                                                               hypothetical protein At2g20010 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-P6D-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: H84583
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-952 <STO>
A;Cross-references: UNIPROT:Q9SL80; UNIPARC:UPI00009F197; GB:AE002093; NID:g4580471; PI
C;Genetics:
A;Gene: A252010
A;Map position: 2
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A; Accession: S75514
A; Accession: L420 «KAN»
A; Residues: 1-420 «KAN»
A; Residues: 1-420 «KAN»
A; Cross-references: UNIPROT: P74004; UNIPARC: UPI0000003509; EMBL: D90911; GB:AB001339; NID
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Start codon: GTG
C; Superfamily: sensory transduction system regulatory protein; response regulator homolo
C; Superfamily: sensory transduction system regulatory protein; response regulator homolo
C; Reywords: phosphoprotein
F; 33-146/Domain: response regulator homology «RRH»
F; 85/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gensory transduction histidine kinase slr1324 - Synechocystis sp. (strain PCC 6803)
NyAlternate names: protein slr1324
C;Speciaes Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75514
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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101 GSEENESSESRLIHDELTQGSSSSLKKKARKQLLMLVBELTNLREYIHIN-
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                                                                                                                                     100 ASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDML
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.G. Contents: annotation A59328
A; Contents: annotation A59328
A; Contents: annotation C.G. Contents: A; descripts A; descr
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-574 < KOH>
A;CHOSS-references: UNIPROT:P23533; UNIPARC:UPI000013287C; GB:M69050; NID:g153073; PIDN:
B;Eisermann, R.; Fischer, R.; Kessler, U.; Neubauer, A.; Hengstenberg, W.
Eur. J. Blotchem. 197, 9191
A;Title: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system. Purific equencing of the ptsH gene.
A;Reference number: S15367; MUID:91200066; PMID:1901791
A;Accession: S17075
A;Status: preliminary
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A,Residues: 1-90 <EIS>
A,Cross-references: UNIPARC:UPI000017007F; EMBL:X60766; NID:g46907; PIDN:CAA43176.1; PID
C,Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I hc
C,Keywords: phosphotrotein; phosphotransferase; sugar transport system
F;5-563/Domain: phosphotransferase system enzyme I homology <PT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphotransferase system enzyme I (EC 2.7.3.9) - Staphylococcus carnosus C; Species: Staphylococcus carnosus C; Species: Staphylococcus carnosus C; Species: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004 C; Date: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004 C; Date: 10-Jul-2004 C; Distermann, R.; Hengstenberg, W. Bacteriol. 174, 2208-2214, 1992 A; W. Bacteriol. 174, 2208-2214, 1992 A; Paritle: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: molecul studies of the gene product. MID:92202148; PMID:1551842 A; PACCESSION: B42374
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10.6%; Score 77.5; DB
Best Local Similarity 24.8%; Pred. No. 33;
Matches 35; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.6%; Score 77.5; DB
Best Local Similarity 31.1%; Pred. No. 7.8;
Matches 28; Conservative 17; Mismatches
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internalin, peptidoglycan bound protein (LPxTG motif) homolog lmo0409 [imported] - List C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: ABI126 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke S;Glance-Sernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 89-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Nok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Accession: ABI126 A;Accession: ABI126 A;Accession: ABI126 A;Accession: ABI126 A;Accession: ABI126 A;Accession: Ballocker DNA A;Residues: 1-821 cqLA> A;Esterimertal source: Etrain EGD-e C;Generical Source: Etrain EGD-e C;Generical Source: Etrain EGD-e
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NyAlternate names: Mypothetical protein TBR8444; hypothetical protein YBR8444; hypothetical protein Stading Secheromyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: Saccharomyces cerevisiae
C;Accession: Stading Sequence revision 01-Sep-1995 #text_change 05-Oct-2004
C;Accession: S54039; SS8835; SG1744; S67871
R;Hunt, S.; Bowman, S.; Harris, D.
R;Hunt, S.; Bowman, S.; Harris, D.
A;Rcession: S54039
A;Rcession: S54039
A;Rcession: S54039
A;Rcession: S54039
A;Rcession: S5803
A;Rcession: S58035
A;Rcession: S61744
A;Rbrandt, P.; Rublow, S.; Otto, B.; Bloecker, H.
Yeast 12, 85-90, 1996
A;Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacchar, R;Refauce number: S61741; MUID:96381250; PMID:8799263
A;Rcession: S61744
A;Residues: 1-444
A;Rbloecker, H.; Brandty
A;Rocession: S61744
A;Residues: 1-444
A;Rbloecker, H.; Brandty
A;Roces-the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Roces-the nucleotide sequence batabase, July 1996
A;Reference number: S67587
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Best Local S
Matches 41
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A;Accession: S67871
A;Molecule type: DNA
A;Residues: 1-444 <a href="https://docume.com/residues/">docume.com/residues/<a href="https://docume.com/residues/">d
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Job time : 30.4055 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

4, 2006, 21:47:48; Search time 144.502 Seconds (without alignments) 707.961 Million cell updates/sec Run on:

US-10-623-189-2 Perfect score: Title:

1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC BLOSUM62 Scoring table: Sequence:

145

2166443 segs, 705528306 residues Gapop 10.0 , Gapext 0.5 Searched: 2166443 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:*
2: uniprot_trembl:* UniProt 05.80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	homo		pan t		Q95234 pongo pygma	_		Q6t8r8 bubalus bub		prop	Bus		•	_	Q4vw71 ctenopharyn	mus	-			Q411m8 cyprinus ca		_		rattus			-	_	aristi	canis	Q9tu09 equus cabal
ID	OB HUMAN	Q6NTS8 HUMAN	OB PANTR	OB_GORGO	OB_PONPY	OB_MACMU	OB_FELCA	QeTere BUBBU	OB BOVIN	OB_BUBBU	OB_PIG	QSTIL9 PIG	OB SHEEP	QSEAE4 BOVIN	Q4VW71 CTEID	OB MOUSE	Q544U0 MOUSE	Q4VW70 HYPMO	Q4VW72_CARAU	Q4L1M8_CYPCA	OB CHICK	Q4VW67 MEGAM	Q4VW68 SILAS	OB RAT	Q4VW66 9PERC	Q4VW81 9TELE	Q4VW60 ANAPL	OB MELGA	Q4VW69 ARINO	OB_CANFA	OB_HORSE
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% Query Match	98.6	98.6	98.2	97.5	96.5	89.8	85.3	83.8	83.8	83.8	83.7	83.7	83.2	83.2	82.6	82.6	82.6	82.0	82.0	82.0	81.7	81.6		80.6		80.5	80.4	80.3	φ.	79.4	69.4
Score	720.5	720.5	717.5	712.5	705.5	656.5	623.5	612.5		612.5	611.5	611.5	608.5	608.5	603.5	603.5	603.5		599.5		597	596.5	593.5	589.5	588.5	588.5	588	587	581.5	580.5	507
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NUCLEOTIDE SEQUENCE

Q9xsw9 sminthopsis Q861r2 bubalus bub Q4vyb6 phodopus ca Q8mk60 alopex lago Q8mk59 nyctereutes Q8mk59 nyctereutes Q8mk1 camis famil Q56Gp8 ovia aries Q766dp halichoerus Q706d1 phoca vitul Q86687 bubalus bub Q8661 camelus dro Q95mg5 capra hircu
0B SMICR Q861R2 BUBBU Q47VE6 9RODE Q40K5 0 ALOLA Q8MK5 0 ALOLA Q8MK5 1 CANPA Q8MK5 1 CANPA Q56QP8 SHEEP Q56QP8 SHEEP Q56QP8 SHEEP Q56QP8 SHEEP Q56QP8 SHEEP Q66QP8 SHEEP Q6
40000000044000
167 118 118 118 118 118 1109 109
6 6 7 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
4 4 444 0 0 0 0 4 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                  P41159; O15158; O56A88; O15158; O56A88; O1-FBB-1995 (Rel. 31, Created) O1-FBB-1995 (Rel. 31, Last sequence update) O1-FBB-1995 (Rel. 48, Last annotation update) Leptin precursor (Obesity factor) (Obese protein) Mame-LBP; Synonyms-OB; Homo eaplens (Human).
                  167 AA
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                  PRT;
                  STANDARD;
                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                      OB HUMAN
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HUMAN
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      TISSUB-Placenta;

MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUB-Placenta;

MEDLINE-213825;

PubMed-12477932; DOI=10.1073/pnas.242603899;

MEDLINE-213825;

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                                                                                                Diabetes 45:675-678(1996)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"A leptin missense mutation associated with hypogonadism and morbid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
Pfam; PR0495; LEPTIN;
PRODOM; PB005698; LEPTIN; 1.
3D-structure; Diabetes mellitus; Disease mutation; Obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR 004196.
V -> M (in dbSNP:17151919).
/FTId=VAR 004197.
R -> W (in morbid obesity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in 30% the clones).
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/FTId=VAR 008094.
VT -> M (in dbSNP:1800564).
/FTId=VAR 011955.
Q -> R (in Ref. 8).
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GO; GO:0006112; P:energy reserve metabolism; TAS.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
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EMBL; U4365; BAA08481; -; mRNA.
EMBL; U4365; AAC50400.1; -; mRNA.
EMBL; U43415; AAC51660.1; -; Genomic_DNA.
EMBL; D63110; BAA09787.1; -; Genomic_DNA.
EMBL; AF008123; AAA83507.1; -; Genomic_DNA.
EMBL; AF008123; AAA81413.1; -; Genomic_DNA.
EMBL; AC068373; AAA81413.1; -; Genomic_DNA.
EMBL; BC0608452; AA46452.1; -; mRNA.
EMBL; BC069517; AAH6952.1; -; mRNA.
                       "A novel polymorphism in the leptin gene.";
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PIR; 133166; 153166; 153166.
PDB; 1AX8; X-ray; @=22-167.
Ensembl; ENSG0000174697; Homo sapiens.
HGNC; HGNC; 553; LEP.
MIM; 164160; -
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Bartholomew D.W., McClellan J.M.;
                                                                                    VARIANT MORBID OBESITY TRP-105
                                         Hum. Mutat. 12:220-220(1998).
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

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Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smilus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                              60 YOOILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                              82 YQQILTSMPSRNVIQISNDLENLRDLIHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
                                                                                29
                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                           Gaps
                                                           1;
                                   DB 1; Length 167;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL, BC063323, AAH69323.1; -; mRNA.
HSSP, P41159; 1AX8.
SMR, Q6NT58; 24-167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                           ö
                                   Score 720.5; DB 1
Pred. No. 2.1e-58;
0; Mismatches 0
                                                                                                                                                                                                                                                               167 AA
                                                                                                                                                                              TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                      Created)
                                  98.68;
                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rescued clones;
                                                                                                                                                                                                                                                                 QENTS8 HUMAN PRELIMINARY;
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
TISSUE=PCR rescued of
                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                           Matches 145;
                                                                                                                                                                               120
                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                       Name=LEP;
                                     Query Match
                                                                                                                                                                                                                                                      HUMAN
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   HELIX
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YQQILTSMPSRNVIQISNDLENLRDLLHVLARSKSCHLPWASGLETLDSLGGVLEASGYS 119
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-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LDB may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.JUL-1998 (Rel. 36, Created)
15.JUL-1998 (Rel. 36, Last sequence update)
10.MAY-2005 (Rel. 47, Last annotation update)
Leptin (Obesity factor).
Name=LEP; Synonyms=OB;
Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLBASGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X., Rockey P.K., Rosteck P.R., "Control of Obese genes from different species: a comparison of closes genes from different species: a comparison of gene structures and the sequences of the obese gene products,
                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                          Score 720.5; DB 2; Length 167;
Pred. No. 2.18-58;
0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                 PRINTS; PR00495; LEPTIN.
ProDom; PD005699; Leptin; 1.
SEQUENCE 167 AA; 18613 MW; BEIA046FFB1554DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULĀR LOCATION: Secreted (Probable). SIMILARITY: Belongs to the leptin family.
Ensembl; ENSG00000174697; Homo sapiens.
G0; G0:0005576; C:extracellular region; IEA.
G0; G0:0005179; P:hormone activity; IEA.
G0; G0:0007165; P:signal transduction; IEA.
InterPro; IPR012251; Cytokine 4 hlx.
InterPro; IPR000065; Leptin.
PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
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InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U96450; AAB54023.1; -; mRNA.
HSSP; P41159; 1AX8.
                                                                                                                                                                                                                                                                                                                                                                        98.64;
                                                                                                                                                                                                                                                                                                                                                                                                       98.38;
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.3'
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; 002750; 3-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9598;
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                                                                                                    YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                  61 YQQILTSMPSRNMIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=LEP; Synonyms=OB;
Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                               VPIQKVQDDTKTLIKTIVTRISDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
Rockey P.K., Rosteck P.R.;
"Cloning of obese genes from different species: a comparison of a
gene structures and the sequences of the obese gene products,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.5%; Score 705.5; DB 1; Length 146; Best Local Similarity 96.6%; Pred. No. 4.3e-57; Matches 141; Conservative 2; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
3F50A13338FFDBD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELLULAR LOCATION: Secreted (Probable).
SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation update)
Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                                                                                                         146
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HSSP, P41159; 1AX8.
SMR; Q95234; 3-146.
Interpro; IPR012351; Cytokine_4_hlx.
Interpro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
                                                                                                                                                                                                                                         TEVVALSRLQGSLQDMLWQLDLSPGC 145
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9600;
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Q95234;
01-NOV-1997 (
01-NOV-1997 (
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                      60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                                                                                                                                                                              61 YQQILTSMPSRNMIQISNDLENLRDLHYLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
                                                                                                                                                                                                                               1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D.P., Zhang X., Hsiung H.M.;
"Gorilla leptin genomic sequence.";
"Usualitied (CT-1996) to the EMBL/GenBank/DDBJ databases.
"Leptin genomic as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LBP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                               1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                    Gaps
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                                                                                                                            98.2%; Score 717.5; DB 1; Length 146; 98.6%; Pred. No. 3.4e-58; tive 1; Mismatches 0; Indels 1
                                                     By similarity. 02C42A06B554D55C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02C43BF6B9A4C85C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 slmilarity).
SUBCELLULAR LOCATION: Secreted (Probable)
SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity
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HSSP; P41159; 1AX8.
                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TEVVALSRLOGSLODMLWQLDLSPGC 145
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR010355; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA; 16031 MW;
                                                                          16059 MW;
ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD005698; Leptin; 1.
                                                                                                                       Query Match
Best Local Similarity 98.6'
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=LEP; Synonyms=OB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 143, Conservat
                                                  96 1
146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9595;
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DISULFID
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                                               DISULFID
                                                                             SEQUENCE
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                             Obesity
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HSSP; P41159; 1AX8
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                                                                                                                         FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            removed.
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Q9N2C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6T8R8_BUBBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDRLGGVLEASGYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 VPIQKVQSDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPVLTLSQMDQTLAI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monkeys. Effects of insulin, body weight, and non-insulin-dependent diabetes mellitus.";

J. Biol. Chem. 271:25331(1996).

- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

- SUBCELLULAR LOCATION: Secreted (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Adipose tissue;
MEDLINE-96411743; PubMed-8810296; DOI=10.1074/jbc.271.41.25327;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Nicolson M.A.,
Hansen B.C.;
                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleo
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leptin.
By similarity.
E7D9F30628A5BBE9 CRC64;
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Pred. No. 1.7e-52;
8; Mismatches 5
                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leptin precursor (Obbesity factor).
Mane=LEP; Synonywas=OB;
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                           167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
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                                            120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                  EMBL; U58492; AAC50730.1; -; mRNA.
HSSP; P41159; 1AX8.
SWR; Q28504; 24-167.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AA; 18953 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
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                                                                                                                                                                                           STANDARD;
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167
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NUCLEOTIDE SEQUENCE.
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Matches 132;
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                                                                                                                                                                                           OB MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.

TISSUE=White adipose tissue;

Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;

Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;

"Molecular cloning of feline leptin cDNA.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LBP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVAGLDFIPGLHPVLSLSKMDQTLAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Secreted (Probable).
SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leptin precursor (Obesity factor).
Pelis silvestris catus (Cat).
                                                                                                                                                                                   167 AA
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By similarity
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142 TEVVALSRLQGSLQDMLWQLDLSPGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012055; Leptin.
PENTER; PTHR1724; Leptin; 1.
PENTER; PTHR1724; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB041360; BAA95481.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 167 B
167 AA; 18584 MW;
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ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                      STANDARD;
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long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fitzelmons C.J., Schmutz S.M.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CMS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintenin constency of the adipose mass.

-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                   Liefers S.C.; "Genotype effects of bovine leptin mutations on pre- and postpartum
                                                                                                                                                                     Konfortov B.A., Licence V.E., Miller J.R.; "Resequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96269621; PubMed-8661738; DOI=10.1007/8003359900118; Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.; "Chromosomal localization of the bovine obesity (OBS) gene."; Mamm. Genome 7:398-399(1996).
                                                                                                                                               MEDLINE=20063685; PubMed=10594237; DOI=10.1007/8003359901180;
                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE OF 46-145.
Lien S., Sundvold H., Klungland H., Vaege D.I.;
"Two novel polymorphisms in the bovine obesity gene (OBS).";
Anim. Genet. 28:245-245(1997).
                    TISSUE=White adipose tissue;
Kawakita Y., Abe H., Miyashige T.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           leptin concentrations.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                      NUCLECTIDE SEQUENCE, AND VARIANTS CYS-25 AND VAL-80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U43943; AAA85906.1; -; MRNA.
EMBL; U50365; AAB61244.1; -; Genomic_DNA.
EMBL; U65793; AAB6579.1; -; mRNA.
EMBL; AA132764; CAB419750.1; -; mRNA.
EMBL; AJ132764; CAB419750.1; -; Genomic_DNA.
EMBL; AJ21648; CAB38018.1; -; Genomic_DNA.
EMBL; AJ512639; CAD54745.1; -; Genomic_DNA.
EMBL; AJ1369; CAD54745.1; JOINED; Genomic_DNA.
EMBL; U4383; AAB18762.1; -; Genomic_DNA.
EMBL; U43833; AAB18762.1; -; Genomic_DNA.
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By similarity.
R -> C.
A -> V.
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HSSP; P41159; 1AX8.
SMR; P50595; 24.167.
Interpro; IPR0121351; Cytokine_4_hlx.
Interpro; IPR0010065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE, AND VARIANT CYS-25
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                                                                                                                                                                                                                                    Mamm. Genome 10:1142-1145(1999).
NUCLEOTIDE SEQUENCE OF 22-167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF02024; Leptin; 1
PRINTS; PR00495; LEPTIN.
ProDom; PD005689; Leptin; 1.
Obesity; Polymorphism; Signal, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 60-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  removed.
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use as
61 YQQILTSLPSRNVVQISNDLENLRDLLHLLAASKSCPLPQVRALESLESLGVVJEASLYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VPIRKVQDDTXTLIXTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLLSLSKMDQTLAI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.8%; Score 612.5; DB 2; Lengua
86.3%; Pred. No. 1.7e-48;
wismarches 9; Indels
                                                                                                                                                                                                                                                                            TISSUE-Adipose tissue;
Rajendran S., Shukla D.C., Saravanan B.C.;
"Cloning and sequencing of buffalo leptin gene.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY427959; AAR05862.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ji S., Spurlock M.E.;
"Partial cloning of bovine obesity gene.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBU databases.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tellam R.L., Briscoe S., Vuocolo A.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1 1 SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;
                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OB BOVIN
P50595; 097918; 095133; 097829;
P0072-1996 (Rel. 34, Created)
O1-0CT-1996 (Rel. 34, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Leptin precursor (Obesity factor).
Bos taurus (Bovine).
146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     SMR; Q6TBRB; 3-146.
GO; G0:0005576; C:extracellular region; IEA.
GO; G0:0005179; F:hormone activity; IEA.
GO; G0:0007165; P:signal transduction; IEA.
InterPro; IPR000065; Leptin.
PF02024; Leptin; 1.
                                                                                                      Leptin (Fragment).
Bubalus bubalis (Domestic water buffalo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; Frecors, ~r.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.3%.
Matches 126, Conservative
Q6T8R8 BUBBU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        P41159; 1AX8.
                                                                                                                                                                                                           NCBI_TaxID=89462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                           22 VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLLSLSKMDQTLAI
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                                                      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDPIPGLHPILTLSKMDQTLAV
Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Landrace;
Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stranzinger G.; "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";
   ä
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Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=White adipose tissue;
MEDLINE=97009821; PubMed=8856925;
Neuenschwander S., Rettenberger G., Meijerink B., Jorg H.,
9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lopes P.S.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Meishan;
Dai R., Li N., Hu X., Wu C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spurlock M.E.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q29406; O19095; Q95251;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leptin precursor (Obesity factor).
Name-LEP; Synonyms-OB, OBS;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AA
   10; Mismatches
                                                                                                                                                                                                                                                                                                 120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 15-110.
   126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bidwell C.A., Ji S.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramsay T.G., Yan X.;
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis C.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OB PIG
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
OB_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                          60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                                                                                                                                                                                                            82 YQQILTSLPSRNVVQISNDLENLRDLIHLLAASKSCPLPQVRALESLESLGVVLBASLYS 141
                                                                                                                                                                                                                                                                     22 VPIRKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLLSLSKMDQTLAI 81
                                                                                                                                                                                                                                          1 VPIQKVQDDTKTLIKTLVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anim. Genet. 35:462-463(2004).

-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15566470; DOI=10.1111/j.1365-2052.2004.01186.x; Vallinoto M., Schneider M.P., Silva A., Iannuzzi L., Brenig B.; "Molecular cloning and analysis of the swamp and river buffalo leptin
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-LEF; Synonyms-OB;
bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                7;
                                                                                                                      83.8%; Score 612.5; DB 1; Length 167;
86.3%; Pred. No. 2e-48;
ive 10; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 612.5; DB 1; Length 167; Pred. No. 2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leptin.
By similarity.
8524749CD69CAD99 CRC64;
      25 25 R -> Q (in Ref. 2).
166 166 G -> E (in Ref. 2).
167 AA; 18716 MW; 94C666B3069E50B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARILY. Secreted (Probable). SUMBLELLULAR LOCATION: Secreted (Probable). SIMILARITY: Belongs to the leptin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leptin precursor (Opesity factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AX495587; AAS86311.1; -; Genomic_DNA.
SMR; O5J732; 24-167.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
PANTHER; PTHR11724; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TEVVALSRLOGSLODMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pecora: Bovidae; Bovinae; Bubalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18688 MW;
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86.3%;
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ProDom; PD005698; Leptin; 1.
                                                                                                                                                        Best Local Similarity 86.3%
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
                                                                                                                                                     Similarity
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB BUBBU
Q5<u>J</u>732;
      CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 YQQILTSLPSRNVIQISNDLENLRDLHLLASSKSCPLPQARALETLESLGGVLBASLYS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VPIQKVQDDTKTLIKTIVTRINDISH-TSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                    22 VPIWRVQDDTKTLIKTIVTRISDISHMQSVSSKQRVTGLDFIPGLHPVLSLSKMDQTLAI
              D'Andrea M., Pilla F., Archibald A.L.;

"Structural and expression analysis of Leptin and Melanocortin-4 sceptor genes in Casertana Bwine breed.";

submitted (NOV-2004) to the BMBL/GenBank/DBJ databases.

EMBL; AJ865080; CAI23842.1; -; Genomic_DNA.

SWR; OFTIL9; 24-167.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000065; Leptin.

PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                              DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simmons J.M., Dyer C.J., Keisler D.H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              22 167 leptin.
167 AA; 18661 MW; 27550E1E0E63814E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  9.
                                                                                                                                                                                                                                                                                                                                           83.7%; Score 611.5; DB 2
86.3%; Pred. No. 2.4e-48;
ive 10; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OB SHEEP STANDARD; PRT; 146 AA. 028603; P79212; 01-NOV-1997 (Rel. 35, Created) 15-UL-1998 (Rel. 36, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Leptin (Obesity factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                         Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 TEVVALSRLÓGALÓDMIROLDISPGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEVVALSRLQGSLQDMLWQLDLSPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 9-125.
                                                                                                                                                                                                                     PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                    Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Adipose tissue;
Simmons J.M., Dyer C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=LEP; Synonyms=OB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VPIQKVQDDTKTLIKTIVTRINDISH-TSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 VPIWRVQDDTKTLIKTIVTRISDISHMQSVSSKQRVTGLDFIPGLHPVLSLSKMDQTLAI 81
Anim. Genet. 27:275-278 (1996).

-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LBP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to mainteain constancy of the adipose mass.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa domestica (domestic pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.7%; Score 611.5; DB 1; Length 167;
86.3%; Pred. No. 2.4e-48;
ive 10; Mismatches 9; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
AV -> GP (in Ref. 8).
I -> L (in Ref. 8).
A -> R (in Ref. 4).
N; 27550EIEOEG3814E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                            EMB1, AP0226976; AAB82724-11; -; mRNA.
EMB1, AP0226976; AAB89724-11; -; mRNA.
EMB1, AR052691; AAC06303.11; -; Genomic_DNA.
EMB1, AR77387; AAC06303.11; -; mRNA.
EMB1, AR477387; AAL084792.11; -; mRNA.
EMB1, AR477386; AAL084792.11; -; mRNA.
EMB1, D4912; AAC48641.11; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEVVALSRLOGALODMLROLDLSPGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leptin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR000065; Leptin.
PANTHER; PTH811724; Leptin; 1.
Pfem; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                         EMBL; U63540; AAB05923.1; -; mRNA.
EMBL; U59894; AAB03458.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 PIG
QETIL9 PIG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00495; LEPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
167
167
22
97
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97
122 1
167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus.
NCBI_TaxID=9825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obesity; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 126;
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CONFLICT
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**Gaps** 

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Query Match
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the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                    60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-Pooled;
Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
Rarhay G.P., Sonelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21180013; PubWed=11282978; DOI=10.1101/gr.170101; Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T., Casas B., Wray J.B., White J., Cho J., Pahrenkrug S.C., Bennett G.Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J., Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Luurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle.";
                                                                                                                                                                                                                                                              83.2%; Score 608.5; DB 1; Length 146; 86.3%; Pred. No. 3.9e-48; ive 9; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BT020625; AAX08642.1; -; mRNA.
                                                                                                                                                                                      96 146 By similarity.
65 65 L -> H (in Ref. 2).
92 92 A (in Ref. 2).
124 124 V -> L (in Ref. 2).
146 AA, 16054 MW, 19D54C53240968CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TEVVALSRLÓGSLÓDMLROLDLSPGC 146
                                                                                               InterPro; IPR012351; Cytokine_4_hlx.
InterPro; PR0000065; Leptin.
PATHER; PTHR11724; Leptin; 1.
Pfam; PF02024; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                EMBL; U84247; AAB41786.1; -; mRNA,
ERBL; U62123; AAB51033.1; -; mRNA,
HSSP, P41159; 1AX8.
SMR; Q28603; 3-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 11:626-630(2001).
                                                                                                                                                              ProDom; PD005698; Leptin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSEAE4 BOVIN PRELIMINARY;
QSEAE4;
10-MAY-2005 (TEBMBLrel. 30,
10-MAY-2005 (TEBMBLrel. 30,
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                  PRINTS; PR00495; LEPTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pooled
                                                                                                                                                                                                                                                                                Best Local Simi
Matches 126;
                                                                                                                                                                           Obesity.
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLPQTSGLQKPESLDGVLBASLYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YOQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 YQQILTSLPSRNVVQISNDLENLRDLHHLLAASKSCPLPQVRALESLESLGVVLEASLYS 141
                                                                                                                                                                                                                                                                                                                                                                    53
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                                                                                                                                                                                                                                                                                                                                                                                                 22 VPICKVQDDTKTLIKTIVTRINDISHTQSVSSKQRVTGLDFIPGLHPLLSLSKMDQTLAI
                                                                                                                                                                                                                                                                                                                                                              1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
05-86 protein (Fragment).
Ctenopharyngodon idella (Grass carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Ctenopharyngodon.
1011—1259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dai H., Long L.; "The squence analysis of the obese gene from the "Molecular cloning and sequence analysis of the obese gene from the Ctenopharyngodom idellus."; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databsses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                     DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 146;
                                                                                                                                                                                                                                                  83.2%; Score 608.5; DB 2; Length
86.3%; Pred. No. 4.6e-48;
ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                             167 AA; 18663 MW; C9AA16B31AF229CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.2%; Pred. No. 1.1e-47;
Matches 123; Conservative 13; Mismatches 9.
                                IEA.
SMR; QSEAE4; 24-167.
GO; GO:005576; C:extracellular region; IEA
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0001465; P:signal transduction; IEA.
InterPro; IPR000065; Leptin.
Pfam; PR02044; Leptin.
PRINTS; PR00495; LEPTIN.
SEQUENCE 167 AA; 18663 MW; C9AA16B31AF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TEVVALSRIQGSIQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 TEVVALSRLQGSLQDMLRQLDLSPGC 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: May 4, 2006, 21:57:12
Job time : 145.502 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
TISSUE=Mesentery adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4VW71_CTEID PRELIMINARY;
                                                                                                                                                                                                                                                                                  Best Local Similarity 86.3
Matches 126; Conservative
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GenCore version 5.1.7
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OM protein - protein search, using sw model

May 4, 2006, 21:52:45; Search time 32.8866 Seconds (without alignments) 364.525 Million cell updates/sec Run on:

US-10-623-189-2 Perfect score:

731 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 145 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 segs, 82675679 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents AA: Database :

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	,	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	, Appl	Appli	Appli	Appli									
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence																
SUMMERTES	ΩI	US-08-347-563A-6	US-08-292-345B-6	US-08-485-942A-6	US-08-488-214A-6	US-08-488-208A-6	US-08-483-211A-6	US-08-488-223A-6	US-08-438-431A-6	US-08-488-225A-6	US-09-204-730B-6	US-09-316-393-6	US-09-686-647A-6	US-08-398-021-3	US-08-788-943A-1	US-08-788-943A-4	US-08-788-943A-5	US-08-823-104-3	US-08-823-104-5	US-08-804-668-1	US-09-003-081-6	US-08-648-262-6	US-08-648-263-6	US-08-674-774-4	US-08-914-375C-32	US-09-172-644-1	US-09-221-178-1	US-09-200-919-1
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	Length DB	166	166	166	166	166	166	166	166	166	166	166	166	146	146	146	146	146	146	146	146	146	146	146	146	146	146	146
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100:0	100.0	100.0	100.0	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6
	Score	731	731	731	731	731	731	731	731	731	731	731	731	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5	720.5
	Result No.	: :	7	٣	4	ĸ	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	, 25	56	27

Appli Appli	Appli Appli Appl	Appli Appli Appli	Appli Appli Appli	Appli Appli Appli	Appli Appli Appli Appli
35	3, 4, 18,	4,4,0,	4,0,0,	4,4,4	444
Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence
PCT-US96-00952-2 PCT-US96-00952-3	US-09-200-919-4 US-08-429-362-3 US-08-823-104-18	US-08-540-242A-4 US-08-347-563A-4 US-09-003-081-5	US-08-292-345B-4 US-08-648-262-5 US-08-648-263-5	US-08-485-942A-4 US-08-488-214A-4 US-08-488-208A-4	US-08-759-628-1 US-08-688-908-7 US-08-483-211A-4 US-08-488-223A-4
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146 146	147 148 148	167 167 167	167 167 167	167 167 167	167 167 167 167
98.6 98.6	98.6 98.6 98.6	98.6 98.6 98.6	98.6 98.6 98.6	98.6 98.6	98.6 98.6 98.6 98.6
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28 29	30 31 32	3 3 3 5 4 5 5 4 5	36 37 38	39 44 14 14	4 4 4 4 6 6 4 8

## ALIGNMENTS

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Sequence 6, Application US/08347563A
Patent No. 5935810
GENERAL INFORMATION:
APPLICANT: THE MCCKEFELLER UNIVERSITY
APPLICANT: THE MCCKEFELLER UNIVERSITY
TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THERAPORDENCE ADDRESS:
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STARE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOCY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position 49
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT PPLICATION DATA:
APPLICATION NUMBER: US/08/347,563A
FLIING DATE: NO. 5935810ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FLIING DATE: August 17, 1994
CLASSIFICATION 514
PRIOR APPLICATION SYSTEM TOWNER: 26,742
REDICATION NUMBER: 26,742
REPERRICE/DOCKET NUMBER: 26,742
REPERRICE/DOCKET NUMBER: 26,742
REPERRICE/DOCKET NUMBER: 301,487-5800
TELEPHONE: 201,487-5800
TELEPRAX: 201,33-1684
TELERX: 133521
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acide
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-347-563A-6
RESULT 1
US-08-347-563A-6
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100.0%; Score 731; DB 1; Length 166; 100.0%; Pred. No. 1e-73;

Query Match Best Local Similarity

Tue May

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Sequence 6, Application US/08485942A

Patent No. 6048837

GENERAL INPORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIVING ZHANG, RICARDO PROENCA,
APPLICANT: JEFFREY M. FRIEDMAN, YIVING ZHANG, RICARDO PROENCA,
APPLICANT: MARCHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
TITLE OF INVENTION: AMENDED)
TITLE OF INVENTION: AMENDED)
TITLE OF INVENTION: AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDPIPGLHPILTLSKMDQTLAVY
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Human ob polypeptide lacking Gln at position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: JUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6048837ember 30, 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION:
PRIOR APPLICATION
142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: OB POLYPEPTID TITLE OF INVENTION: ABENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 166 amino acids
amino acid
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
: USA
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
                                                                                                                          US-08-485-942A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Patent No. 6001968
GENERAL INPORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREG
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                                                                                                                                                                                          61 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                                                                                                                                82 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
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                                                                1 VPIOKVODDTKTLIKTIVTRINDISHTSVSSKOKVTGLDFIPGLHPILTLSKMDOTLAVY 60
                                                                                                            22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 81
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   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,345B
FILING DATE: AUGUST 17, 1994
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: AUGUST 17, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., DAVIG A.
REGISTRATION NUMBER: 26,742
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                        121 EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                                                                                                                                    142 EVVALSRLQGSLQDMLWQLDLSPGC 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 166 amino acids
amino acid
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Best Local Similarity 100.
Matches 145; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack
STATE: New Jerse:
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-292-345B-6
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Matches 145;
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MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
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82 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLBASGYST 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein DESCRIPTION: Human ob polypeptide lacking Gln at position 49
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,208A
FILING DATE: O'-JUM-1995
CLASSIFICATION TOWNER: US/08/488,208A
FILING DATE: O'-JUM-1995
CLASSIFICATION TOWNER: US/485,943
APPLICATION NUMBER: 08/485,943
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
CLASSIFICATION: 514
CLASSIFICATION: 514
CCLASSIFICATION: 514
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Pred. No. 1e-73;
; Mismatches 0;
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                                                                                                                                                                                                       Sequence 6, Application US/08488208A
Patent No. 612448
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACIDS AND PRE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
COUNTRY: New Jersey
COUNTRY: USA
                                                     121 EVVALSRIQGSIQDMLWQLDLSPGC 145
                                                                             142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-08
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; St
Best Local Similarity 100.0%; P:
Matches 145; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
NFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
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                                                                                                                                                                     Sequence 6, Application US/08488214A

Patent No. 6124439

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: (AS AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein DESCRIPTION: Human ob polypeptide lacking Gln at position DESCRIPTION: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAURENT APPLICATION DATA:
APPLICATION UNDER: US/08/488,214A
FILING DATE: UUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6124439ember 30, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600-1-087 CIP 2D
                                                          142 EVVALSRLÓGSLÓDMLWÓLDLSPGC 166
                 121 EVVALSRIQGSLODMIWQLDLSPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          : 411 Hackensack Avenue
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                         Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 166 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Sequence 6, Application US/08488223A
Sequence 6, Application US/08488223A
Patent No. 6350730
GENERAL INFORMATION
APPLICANT: THE ROCKEFELLER UNIVERSITY
APPLICANT: THE ROCKEFELLER UNIVERSITY
APPLICANT: THE ROCKEFELLER UNIVERSITY
ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
                                                                                               61 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                                                                                           92 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 60
                              22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDPIPGLHPILTLSKMDQTLAVY 81
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MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6350730ember 30, 1994
APPLICATION NUMBER: 08/22,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                     142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                        Sequence 6, Application US/08483211A
Patent NO. 6309853
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                    QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                               82 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
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DESCRIPTION: Human ob polypeptide lacking Gln at position 49
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100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,211A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
FILING DATE: May 10, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/39,345
FILING APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
FILING DATE: No. 6309853ember 30, 1994
CLASSIFICATION: 514
FILING DATE: NO. 6309853ember 30, 1994
CLASSIFICATION: 514
ATCHEVATION NUMBER: 08/292,345
FILING DATE: AUGUST 17, 1994
ATCHEVATION: 514
ATCHEVATION NUMBER: 26,742
REGISTRATION NUMBER: 201 487-5800
TELEPRAK: 201 343-1684
                                                                                                                                            142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 166 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                       RESULT 6
US-08-483-211A-6
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Sequence 6, Application US/08488225A

Sequence 6, Application US/08488225A

Patent No. 6471956

GENERAL INFORMATION:
APPLICANT: THE NOCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack Avenue
CITT: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 81
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DESCRIPTION: Human ob polypeptide lacking Gln at position
DESCRIPTION: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTURENT ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CORERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/488,225A
FILING DATE: June 7, 1995
CLASSIFICATION NUMBER: 08/483,211
FILING DATE: June 7, 1995
CLASSIFICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION NUMBER: 08/436
FILING DATE: August 17, 1994
CLASSIFICATION NUMBER: 08/41956ember 30, 1994
CLASSIFICATION NUMBER: 08/41956ember 30, 1994
CLASSIFICATION NUMBER: 20, 41956ember 30, 1994
CLASSIFICATION NUMBER: 08/41956ember 30, 1994
CLASSIFICATION NUMBER: 08/425
ATTORNEY/AGENT INPORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
REFERENCE/DOCKET NUMBER: 201487-5800
TELERHONE: 201487-5800
142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 145; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Huma
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                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08438431A
Patent No. 6429290
GENERAL INPORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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        QOILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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DESCRIPTION: Human ob polypeptide lacking Gln at position 49
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100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,431A

FILING DATE: May 10, 1995

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/347,563

FILING APPLICATION 514

PRIOR APPLICATION 514

PRIOR APPLICATION 1514

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

CLASSIFICATION S14

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 600-1-087 CIPI

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                           142 EVVALSRLQGSLQDMLWQLDLSPGC 166
                                                                                                                           121 EVVALSRLOGSLODMLWQLDLSPGC 145
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
                                                 82 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09204730B
Patent No. 6703493
GENERAL INFORMATION:
APPLICANT: JEFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA
TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
ANAMARIA OF GENERAL OF SA AMENDED)
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MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: Floppy disk
COMPUTER: OF PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/204,730B
FILING DATE: 03-Dec-1998
CLASSIFLATION: <understand the company of the com
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100.0%; Pred. No. 1e-73;
tive 0; Mismatches 0; Indels
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FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087DIV
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                     121 EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                           EVVALSRLQGSLQDMLWQLDLSPGC 145
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
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Best Local Similarity 100.(
Matches 145; Conservative
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US-09-204-730B-6
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Sequence 6, Application US/09316393
| Patent No. 6734160
| CENERAL INFORMATION:
| CENERAL INFORMATION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
| TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THERE NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
DESCRIPTION: Ob protein harboring Gln deletion at position 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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100.0%; Pred. No. 1e-73;
                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EVVALSRLQGSLQDMLWQLDLSPGC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,393
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Patent No. 6821945
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
APPLICANT: Veffrey M. Friedman
APPLICANT: Yiying Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: AUGUST 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amin
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Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                              Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                          07601
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60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
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                                                                                                                                                                                                                                                                             98.6%; Score 720.5; DB 1; Length 146; 99.3%; Pred. No. 1.2e-72; ive 0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08788943A
Patent No. 5831017
GENERAL INFORMATION:
APPLICANT: HOFfmann, James Arthur
TILE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
TILE OF INVENTION: FORMULATIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: /note= "Xaa at position 28 is Gln; OTHER INFORMATION: or absent;" US-08-788-943A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,943A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CALLINGET, Steven P
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X10540
TELEPHONE: (317) 276-0757
TELEPHONE: (317) 277-1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESSEE: Bli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
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TELEPHONE: (317) 277-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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                               TELEFAX: 317-277-1917
INPORMATION FOR SEG ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
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Best Local Similarity 99.3
Matches 145; Conservative
                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
US-08-398-021-3
          TELEPHONE:
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APPLICANT: Ricardo Proenca
APPLICANT: Margherita Maffei
APPLICANT: J. Halaas
APPLICANT: J. Halaas
APPLICANT: Vetan Gajiwala
APPLICANT: Ketan Gajiwala
APPLICANT: Stephen K. Burley
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: WOLLEIC AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: WOMER: US/09/686,647A
CURRENT APPLICATION NUMBER: 09/183,374
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1994-11-30
PRIOR FILING DATE: 1994-08-17
NUMBER OF SEQ ID NOS: 42
SCOFFWARR: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCOMMATION:
APPLICANT: Becker, Gerald W.
APPLICANT: Hacker, Gerald W.
APPLICANT: Hale, John E.
TITLE OF INVENTION: ANTI-OBESITY PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/399,021
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US-08-398-021-3
; Sequence 3, Application US/08398021
; Patent No. 5594101
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ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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LENGTH: 166
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                                                                                                                            1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 59
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                                                  Gaps
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                                                     1;
Score 720.5; DB 1; Length 146;
Pred. No. 1.2e-72;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-788-943A-4
; Sequence 4, Application US/08788943A
; Patent No. 5831017
; GENERAL INFORMATION:
    APPLICANT: Hoffmann, James Arthur
    TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND TITLE OF INVENTION: PORMULATIONS THEREOF;
    TURBE OF INVENTION: PORMULATIONS THEREOF;
    NUMBER OF SEQUENCES: 35
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Eli Lilly and Company
    STREET: Lilly Corporate Center/Patent Division
    CITY: Indianapolis
    STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.6%; Score 720.5; DB 1; Length 146; Best Local Similarity 99.3%; Pred. No. 1.2e-72; Matches 145; Conservative 0; Mismatches 0; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-4M-1997
CLASS!FICATION NUMBER: US/08/788,943A
FILING DATE: 24-4M-1997
CLASS!FICATION: 530
ATTORNEY/AGENT INFORMATION:
NAMME: Caltrider, Steven P
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X.0540
TELEPHONE: 317) 277-1917
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERIESTICS:
LENGTH: 146 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ATRANDEDNESS: single
                                                                                                                                                                                                                                                                                               TEVVALSRLOGSLODMLWOLDLSPGC 145
                                                                                                                                                                                                                                                                                                                           121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
Query Match
Best Local Similarity 99.3%;
Matches 145; Conservative
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MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 28
OTHER INFORMATION:
OTHER INFORMATION:
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Db 61 YQQ1LTSMPSRNVIQISNDLENLRDLAHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Qy 120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
Db 121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
Search completed: May 4, 2006, 21:58:24
Job time: 32.8866 sees
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Sequence 1, Appli
Sequence 211, App
Sequence 1, Appli
Sequence 127, App
Sequence 1, Appli
Sequence 2, Appli
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Sequence 2, A
Sequence 1, A
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Sequence 6,
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Sequence 1,
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Sequence 2
Sequence 1
Sequence 4
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Sequence 1
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                                                                                                         731
1 VPIQKVQDDTKTLIKTIVTR......SRLQGSLQDMLWQLDLSPGC
                                                        ; Search time 112.113 Seconds
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.: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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:: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

:: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

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:: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Match Length
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Sequence 2, Application US/10623189

Sequence 2, Application Wordsolve 1

GENERAL INFORMATION:
APPLICANT: DEPAOLI, Alex M.
APPLICANT: DEPAOLI, Alex M.
APPLICANT: GRAL, Elif Arioglu
APPLICANT: GRAC, Abhimanyu
ITILE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETER
TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
TITLE OF INVENTION NUMBER: US 10/279,129
FRIOR PELLING DATE: 2002-10-22
FRIOR APPLICATION NUMBER: US 60/336,394
FRIOR FILING DATE: 2001-10-22
FRIOR FRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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100.0%; Pred. No. 3.8e-71;
.ive 0; Mismatches 0; Indels
US-10-775-180-168
US-10-775-180-169
US-10-775-180-170
US-10-775-180-171
US-10-775-204-551
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US-11-679-999-18
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; Sequence 6, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INPORMATION:
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Matches 145; Conserv
               LENGTH: 145
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61 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10730488;
Publication No. US20040213763A1
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROBNCA,
MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND
STEPHEN K. BURLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein barboring Gln deletion at position 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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100.0%; Pred. No. 4.6e-71;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: ANGUSE 17, 1994
ATTORNEY GEENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERNICE/DOCKET NUMBER: 600-1-087
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVVALSRLQGSLQDMLWQLDLSPGC 145
                                                  411 Hackensack Avenue
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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amino acid
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TELEX: 13521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
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Best Local Similarity 100.
Matches 145; Conservative
       CORRESPONDENCE ADDRESS: ADDRESSE: Klauber &
                                                                                                New Jersey
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CITY: Hackensack
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US-09-316-393-6
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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                                                                                                STATE: Ne COUNTRY:
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APPLICANT: THE ROCKEFELLER UNIVERSITY TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09316393
Publication No. US20030040039A1
Publication No. US20030040039A1
SEMERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREC
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 731; DB 3; Length 166; Best Local Similarity 100.0%; Pred. No. 4.6e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
APPLICATION NUMBER: 08/347,563
FILING DATE: No. US20020107211Alember 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEFAX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/736,084
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 EVVALSRLQGSLQDMLWQLDLSPGC 145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 166 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                        SEQUENCES: 98
                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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61 QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
DESCRIPTION: Ob protein harboring Gln deletion at position 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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Sequence 1, Application US/10191377
Publication No. US20030099709A1
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
TITLE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
FILE REPERENCE: A-575
CURRENT APPLICATION NUMBER: US/10/191,377
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VET. 2.0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/780,295
FILING DATE: 17-Peb-2004
FILING DATE: 17-Peb-2004
FILING DATE: 17-Peb-2004
APPLICATION NUMBER: US/09/316,393
FILING DATE: 17-August-1999
APPLICATION NUMBER: 08/292,345
FILING DATE: 17-August-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087
TELECOMMUNICATION INPERMATION:
TELEPHONE: 201 487-5800
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100.0%; Pred. No. 4.6e-71;
tive 0; Mismatches 0;
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201 343-1684
TELEX: 133521
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.3
Matches 145; Conservative
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Best Local Similarity 100.
Matches 145; Conservative
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ORGANISM: Human Leptin
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Publication No. US20040214214A1
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
APPLICANT: THE ROCKEFELLER UNIVERSITY
APPLICANT: ACTOR MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position
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                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/730,488
FILING DATE: 08-Dec-2003
CLASSIFICATION: <unimnmon*bridge*CLASTION: <uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 731; DB 4; 100.0%; Pred. No. 4.6e-71;
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/736,084
FILING DATE: 13-Dec-2000
APPLICATION NUMBER: 08/48,431
FILING DATE: May 10, 1995
APPLICATION NUMBER: 08/347,563
FILING DATE: November 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVVALSRLQGSLQDMLWQLDLSPGC 145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO: 6:
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STATE: New Jersey
COUNTRY: USA
                        COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 145; Conservative
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60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
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                                                                                         Length 146;
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                                                                                       98.6%; Score 720.5; DB 4; Length 99.3%; Pred. No. 5.3e-70; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10467114
Publication No. US20040072219A1
GENERAL INFORMATION:
APPLICANT: Carry Francis J.
APPLICANT: Carrer, Graham
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: William, Anita
TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/467,114
CURRENT APPLICATION NUMBER: US/10/467,114
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: BP 01102618.4
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: BP 01103954.2
PRIOR APPLICATION NUMBER: PCT/EP02/01188
PRIOR FILING DATE: 2001-02-19
PRIOR PLING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                             TEVVALSRIQGSIQDMIWQLDLSPGC 145
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GENERAL INFORMATION: APPLICANT KINELER, Olaf
                                                                                       Query Match
Best Local Similarity 99.3
Matches 145; Conservative
                            ; ORGANISM: Homo sapiens
US-10-419-058-2
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US-10-622-998-1
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Publication No. US20030232421A1

Publication No. US20030232421A1

Publication No. US20030232421A1

APPLICANT: HYBRIGARICS, LYNX THERAPEUTICS INC.

APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun Luc

TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)

TITLE OF INVENTION NUMBER: US/10/139,794

CURRENT APPLICATION NUMBER: US 60/288,885

PRIOR APPLICATION NUMBER: US 60/288,885

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ 1D NOS: 2930

SOFTWARE: PatentIn version 3.1
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                                                                 60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
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1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
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Pred. No. 5.3e-70;
0; Mismatches 0; Indels 1
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                                                                                                                                                  120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
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Best Local Similarity 99.3%;
Matches 145; Conservative (
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LENGTH: 146
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US-10-419-058-2
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GENERAL INFORMATION:

APPLICANT: Carre, Graham
APPLICANT: Carre, Graham
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Hamilton, Anita
APPLICANT: MANUNOSENITY
ITILE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
FILE REFERENCE: ADR-125
FILE REFERENCE: 2003-09-25
FILE REPERENCE: 2003-09-25
FRIOR PLILING DATE: 2001-03-09
FRIOR PLILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-15
FRIOR PLILING DATE: 2001-03-15
FRIOR FILING DATE: 2001-03-16
FRIOR FILIN
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Publication No. US20050002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMEIER
APPLICANT: Christian VOETSMEIER
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.0002U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 5.3e-70;
0; Mismatches 0;
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                                                                                      120 TEVVALSRLOGSLODMLWQLDLSPGC 145
                                                                                                                        121 TEVVALSRLQGSLQDMLWQLDLSPGC 146
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Publication No. US20040180386A1
GENERAL INFORMATION:
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ilarity 99.3%;
Conservative (
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US-10-468-496-1
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Best Local Similarity
Matches 145; Conserv
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TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADA
TITLE OF INVENTION: POLYMER
TITLE OF INVENTION: POLYMER
FILE REPENCE: A 82 2
CURRENT APPLICATION NUMBER: US/10/622,998
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR FILING DATE: 2002-07-19
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 1
LENGTH: 146
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98.6%; Score 720.5; DB 4; Length
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 5.3e-70;
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99.3%; Pred. No. 5...
0; Mismatches
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DATABASE ACCESSION NUMBER: Genbank AAA60470
DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211
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Matches 145; Conservative
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US-10-622-998-1
                Ladd, David
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1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROSS, Richard
APPLICANT: ROSS, Richard
APPLICANT: SAYERS, Jon
TILE OF INVENTION: POLYDEPLICAN
FILE REFERENCE: 100042.55084US
CURRENT APPLICATION NUMBER: US/10/502,344
CURRENT FILING DATE: 2004-07-23
PRIOR PLING DATE: 2003-01-24
PRIOR PLING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
LENGTH: 146
                                                                                                                                                                                                   120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
                                                                                                                                                                                                                                                             121 TEVVALSKLÓGSLÓDMLWÓLDLSPGC 146
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Job time: 113.113 secs
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                                                                                                                                                                                                                                                                                                                                                                                               US-10-502-344-22; Sequence 22, Application US/10502344; Publication No. US20050214762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
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Sequence. 1871.

Bublication No. US20050020496A1

GENERAL INFORMATION:

APPLICANT: DEPAOLI, Alex M.

APPLICANT: TAYLOR, Simeon I.

CURRENT APPLICATION NUMBER: US 00,10,23,189

CURRENT FILING DATE: 2000-10-22

PRIOR APPLICATION NUMBER: US 60/336,394

PRIOR FILING DATE: 2001-10-22

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 146
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US-10-623-189-1
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Pred. No. 5.3e-70;
0; Mismatches 0; Indels 1
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CURRENT APPLICATION NUMBER: US/10/872,198
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PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-10
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Matches 145; Conservative (
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Best Local Similarity 99.33
Matches 145; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                        4, 2006, 21:58:39 ; Search time 17.9381 Seconds (without alignments) 374.135 Million cell updates/sec
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1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLQDMLWQLDLSPGC 145
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1: /SIDS5/ptodata/2/pubpaa/US08 NEW PUB.pepl:*
2: /SIDS5/ptodata/2/pubpaa/US06 NEW PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US08 NEW PUB.pep:*
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11: /SIDS5/ptodata/2/pubpaa/US11 NEW PUB.pep:*
12: /SIDS5/ptodata/2/pubpaa/US11 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-176-830-211
US-11-236-198-32
US-10-821-224-1384
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Sequence 663, App
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Sequence 37, Appli
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Sequence 33, Appli
Sequence 34, Appli
Sequence 36, Appli
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                                                                                                                                                                      US-10-926-709-709-709-11-76-830-669
US-11-176-830-669
US-11-236-198-37
US-11-236-198-39
US-11-236-198-39
US-11-236-198-39
US-11-236-198-39
US-11-236-198-39
US-10-926-798-8
US-10-926-798-15
US-10-926-798-16
US-10-926-798-16
   US-11-176-830-663
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US-11-176-830-667
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US-11-236-198-31
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US-10-841-218-1
                                                                                                                                                          US-10-926-798-5
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is Sequence 19, Application US/10519390
is Publication No. USZ0060008872A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
         Best Local Similarity 99.3
Matches 145; Conservative
         9977.5
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US-10-519-390-19
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Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Tabat, Tabat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 YQQILTSMPSRNVIQISNDLENLADLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
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                                                                                                                                                                                                                                                                                                                              22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 81
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                                                                                                            Length 167;
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98.6%; Score 720.5; DB 9; Length:
Best Local Similarity 99.3%; Pred. No. 2.2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      0; Indels
                                                                                                            DB 11;
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; Publication No. US20050272656A1
; GENERAL INFORMATION:
; TILLE OF INVENTION:
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS: 47
; CORRESPONDENCE ADDRESS: 5
; STREET: 460 Point San Bruno Blvd
; STARET: Acouth San Francisco
; STARET: California
                                                                                                     Query Match

98.6%; Score 720.5; DB
Best Local Similarity 99.3%; Pred. No. 2e-64;
Matches 145; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
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TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-236-198-32
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US-11-192-219-47
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                                                                                     Sequence 211, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Guyon, Thierry

APPLICANT: Guyon, Thierry

APPLICANT: Drittenti, Lila

APPLICANT: Weas, Manuel

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (9228)

CURRENT FILING DATE: 2003-07-06

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-03-21

PRIOR PILING DATE: 2003-03-21

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2002-09-09

WUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 1306
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APPLICANT: Erickson, Mary Ruth
APPLICANT: Fruebis, Joachim
APPLICANT: Fruebis, Joachim
APPLICANT: Fruebis, Joachim
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
TITLE OF INVENTION: LSR-Leptin Interaction and Trains Darge: 20.05-09-27
CURRENT TILING DATE: 20.05-09-27
PRIOR PILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA60470
DATABASE ENTRY DATE: 1995-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TEVVALSRLOGSLODMLWOLDLSPGC 145
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Publication No. US20060030530A1
GENERAL INFORMATION:
                                                                     -11-176-830-211
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US-11-236-198-32
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LENGTH: 167
TYPE: PRT
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Sequence 672, Application US/11176830

| Sequence 672, Application US/11176830
| Publication No. US20060020116A1
| GENERAL INFORMATION:
| APPLICANT: Guoto, Thierry
| APPLICANT: Guoto, Thierry
| APPLICANT: Usqu, Manuel
| TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding if TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding if TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding if TITLE OF INVENTION: Acid Molecules and Related Applications
| TITLE OF INVENTION NUMBER: 105610066 |
| FILE REFERENCE: 17109-012002 (922B) |
| CURRENT APPLICATION NUMBER: 10668 |
| PRIOR FILING DATE: 2003-09-08 |
| PRIOR FILING DATE: 2003-03-21 |
| PRIOR FILING DATE: 2003-03-21 |
| PRIOR FILING DATE: 2002-09-09 |
| NUMBER OF SEQ ID NOS: 1306 |
| SEQ ID NO SEQ ID NOS: 1306 |
| TENGRAL SESTER FASTER FASTE
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                                                                                   Length 146;
                                                                                                                                                             0; Indels
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                                                                                          Query Match 98.3%; Score 718.5; DB 1 Best Local Similarity 98.6%; Pred. No. 2.6e-64; Matches 144; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
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Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
, ORGANISM: Homo sapiens
US-11-176-830-666
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Sequence 666, Application US/11176830

Publication No: US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
CURRENT APPLICATION NUMBER: 10/611/176,830

CURRENT APPLICATION NUMBER: 00/457,135

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SENGTH: 146
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98.6%; Score 720.5; DB 11; Length
Best Local Similarity 99.3%; Pred. No. 6.1e-64;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/192,219
FILING DATE: 27-Uu1-2005
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Uun-1996
APPLICATION NUMBER: 08/58505
FILING DATE: 08-Jan-96
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUICATION INFORMATION:
TELEPHONE: 415/22-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TEVVALSRLQGSLQDMLWQLDLSPGC 145
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TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
          ZIP: 94080
COMPUTER READABLE FORM:
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US-11-176-830-666
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Sequence 665, Application US/11176830

| Bequence 665, Application US/11176830
| Publication No. US20060020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier, Rene
| APPLICANT: Gantier, Rene
| APPLICANT: Gantier, Inlary
| APPLICANT: Drittanti, Lila
| APPLICANT: Vega, Manuel
| AP
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Publication No. US20060020116A1

SERENAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Oritanti, Lila
APPLICANT: Usea, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-03-21
                                                    61 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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                                                                                                                                                                                                                                 121 TEVVALSRLQGSLQDMLWQLDISPGC 146
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US-11-176-830-665
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-11-176-830-665
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Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gautier, Rene
APPLICANT: Dritearit, Lila
APPLICANT: Vega, Manuel
ITILE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
ITILE OF INVENTION: Acid Molecules and Related Applications
ITILE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT FILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR FILING DATE: 2003-03-03-21

PRIOR FILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 683

LENGTH: 146

TYPE: PRI
              TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (922B)
CURRENT PAPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR PILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 7 ENGLISH OF TABLES OF TABL
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Pred. No. 2.6e-64;
1; Mismatches 0; Indels 1;
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Pred. No. 2.6e-64;
1; Mismatches 0; Indels 1;
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98.6%;
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Best Local Similarity 98.6%;
Matches 144; Conservative
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Best Local Similarity 98.6
Matches 144; Conservative
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CORGANISM: Homo sapiens
US-11-176-830-677
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US-11-176-830-683
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US-11-176-830-683
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RESULT 14
US-11-176-830-682
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Sequence 673, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gartier, Rene

APPLICANT: Gartier, Rene

APPLICANT: Drittenti, Lila

APPLICANT: Wead, Manuel

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (9228)

CURRENT APPLICATION NUMBER: 10/658 834

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-03-21

PRIOR FILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR PILING DATE: 2003-09-09

NUMBER OF SEC ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
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                                                                                                                                                                                                                                                                     DB 11; Length 146;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                     Query Match 98.2%; Score 717.5; DB 1:
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0
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PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PRECEE FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TEVVALSRLÖGSLÖDMLWQLDLSPGC 146
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US-11-176-830-673
                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-11-176-830-671
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                                                                                                      SEQ ID NO 671
LENGTH: 146
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Sequence 676, Application US/11176830

Sequence 676, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
TITLE OF INVENTION: Asid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (922B)
FILE REFERENCE: 17003-03-09-08
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICA
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Sequence 682, Application US/11176830

Sequence 682, Application No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Garatier, Rene

APPLICANT: Garatier, Lila

APPLICANT: Garatier, Rene

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding h

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

CURRENT PLING DATE: 2005-07-06

FRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-09

PRIOR PILING DATE: 2002-09-09

NUMBER: OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 682

LENGTH: 146

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98.6%; Pred. No. 3.2e-64;
tive 1; Mismatches 0
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Best Local Similarity 98.61
Matches 144; Conservative
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ORGANISM: Homo sapiens
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US-11-176-830-682
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DB 11; Length 146;

98.2%; Score 717.5;

Query Match

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RESULT 13

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RESULT 15
US-11-236-198-36
; Sequence 36, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Bithain, Bernard
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; FILE REFERENCE: 70.052. REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT APPLICATION NUMBER: US/11/236,198
; PRIOR PILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE PATENT
                                                                                                                                                                                 60 YQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
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                                                                                1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 59
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98.2%; Score 717.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1;
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0; Indels
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LENGTH: 146
TYPE: PRT
) ORGANISM: Pan troglodytes
US-11-236-198-36
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